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OM nucleic - nucleic search, using sw model

Run on: July 21, 2004, 11:14:20 ; Search time 1 Seconds
(without alignments)
2.357 Million cell updates/sec

Title: US-10-023-182-1
Perfect score: 752
Sequence: 1 ATCCTGCTGGCCCTGACT.....TAAACTGAGCTACGAAAA 752

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 0.5

Searched: 4 segs, 1567 residues

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : *seq:*
1: /home/sdavid/sdavid-cmp/jul04/davis182/6274145.seq:*
2: /home/sdavid/sdavid-cmp/jul04/davis182/5804381.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	752	100.0	752	1	US-08-937-263B-1
2	752	100.0	752	2	US-08-725-182C-1
3	30.6	4.1	752	1	US-08-937-263B-1
4	30.6	4.1	752	2	US-08-725-182C-1
5	23.6	3.1	32	1	US-08-937-263B-3
6	20.2	2.7	31	1	US-08-937-263B-2
7	12.6	1.7	32	1	US-08-937-263B-3
8	10	1.3	31	1	US-08-937-263B-2

ALIGNMENTS

RESULT 1
US-08-937-263B-1
Sequence 1, Application US/08937263B

Patent No. 6274145
GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander, Knuth; Drifflout, Jan W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA

ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Simn, Eric, Patent Agent
REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 752-5958
TELEFAX: (212) 318-3000
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 752 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-937-263B-1

Query Match 100.0%; Score 752; DB 1; Length 752;
Best Local Similarity 100.0%; Pred. No. 0.003;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	ATCCTGCTGGCCCTGACTCTTCTCTGAGAGCCGGGACAGAGCTCCGAGCCATGCAGG	60
Db	1	ATCCTGCTGGCCCTGACTCTTCTCTGAGAGCCGGGACAGAGCTCCGAGCCATGCAGG	60
Qy	61	CCGAGGCGCGGGACAGAGGGGTTTCAACGGGCGATGCTGAGGCCAGAGGCTCTTGCA	120
Db	61	CCGAGGCGCGGGACAGAGGGGTTTCAACGGGCGATGCTGAGGCCAGAGGCTCTTGCA	120
Qy	121	TTCTGATGGCCCAAGGGGGCAATGCTGGCGGCCCAAGAGGGGGTCCACCGGGCGGCA	180
Db	121	TTCTGATGGCCCAAGGGGGCAATGCTGGCGGCCCAAGAGGGGGTCCACCGGGCGGCA	180
Qy	181	GAGGTCCCGGGGCGAGGGGGCAAGGGCTCGGGGCGGGAGGAGGCGCCCGCGGG	240
Db	181	GAGGTCCCGGGGCGAGGGGGCAAGGGCTCGGGGCGGGAGGAGGCGCCCGCGGG	240
Qy	241	GTCGCAATGGCGCGCGCTTCAAGGGCTGAATGATGCTGACAGATGCGGGGCAAGGGGGC	300
Db	241	GTCGCAATGGCGCGCGCTTCAAGGGCTGAATGATGCTGACAGATGCGGGGCAAGGGGGC	300
Qy	301	CGAGAGCGCCCTGCTTGAATTTTACTCGCCATGCTCTTTCGGGACACCCATGAGACAG	360
Db	301	CGAGAGCGCCCTGCTTGAATTTTACTCGCCATGCTCTTTCGGGACACCCATGAGACAG	360
Qy	361	AGCTGGCCCGCAGAGGCTGGCCAGAGATGCCACCGCTTCCCGTCCAGGGGTGCTTC	420
Db	361	AGCTGGCCCGCAGAGGCTGGCCAGAGATGCCACCGCTTCCCGTCCAGGGGTGCTTC	420
Qy	421	TGAAGAGTTCACTGTGTCGGGCAACATGACTGATCTGACGTGCTGACAGCACCC	480
Db	421	TGAAGAGTTCACTGTGTCGGGCAACATGACTGATCTGACGTGCTGACAGCACCC	480
Qy	481	GCCAGTCGACGCTCTCATAGCTCTGCTTCCAGAGAGCTTCCCTGTTGATGTGATCA	540
Db	481	GCCAGTCGACGCTCTCATAGCTCTGCTTCCAGAGAGCTTCCCTGTTGATGTGATCA	540
Qy	541	CGAGTCCTTTCGCGCGTGTGTTTGGCTCAGGCTCCCTCAGGAGAGAGGCGCTAAGCC	600
Db	541	CGAGTCCTTTCGCGCGTGTGTTTGGCTCAGGCTCCCTCAGGAGAGAGGCGCTAAGCC	600
Qy	601	AGCCTGGCGCCCTTCTAGATGATGCTCTCCCTAGGAAATGATCCAGACGAGTG	660
Db	601	AGCCTGGCGCCCTTCTAGATGATGCTCTCCCTAGGAAATGATCCAGACGAGTG	660

Db 601 AGCTGCGGCCCTTCTAGTCAATGCTCTCCCTAGAGGATGTCCTCCACAGCAGTG 660
Qy 661 GCCAGTTCATTTGGGGGCTGATTTGTTGCTGAGAGAGCGCTTACATGTTTGT 720
Db 661 GCCAATTCATTTGGGGGCTGATTTGTTGCTGAGAGAGAGCGCTTACATGTTTGT 720
Qy 721 TTCTGTAGAAAATAAACTGAGCTACGAAAA 752
Db 721 TTCTGTAGAAAATAAACTGAGCTACGAAAA 752

RESULT 2

US-08-725-182C-1
; Sequence 1, Application US/08725182C
; Patent No. 5804381
; GENERAL INFORMATION:
; APPLICANT: Yao-Tseng Chen, Scanlan, Matthew, Gure, Ali,
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE ENCODING
; TITLE OF INVENTION: AN ESOPHAGEAL CANCER ASSOCIATED ANTIGEN, THE ANTIGEN ITSELF,
; NUMBER OF SEQUENCES: 1
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Felfe & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/725,182C
; FILING DATE: 03-October-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 5804381man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-725-182C-1

Query Match 100.0%; Score 752; DB 2; Length 752;

Best Local Similarity 100.0%; Pred. No. 0.003; Indels 0; Gaps 0;

Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATCTCTGAGGCGCTTCTCTCTGAGAGCCGCGGAGAGAGGCTCCGAGGCAATGACAG 60
Db 1 ATCTCTGAGGCGCTTCTCTCTGAGAGCCGCGGAGAGAGGCTCCGAGGCAATGACAG 60
Qy 61 CCGAAGGCGCGGCGCAGGCGGCTTGAAGCGGCGATGCTGATGCGCCAGAGAGGCTTGCA 120
Db 61 CCGAAGGCGCGGCGCAGGCGGCTTGAAGCGGCGATGCTGATGCGCCAGAGAGGCTTGCA 120
Qy 121 TTCTGTAGAAAATAAACTGAGCTACGAAAA 180
Db 121 TTCTGTAGAAAATAAACTGAGCTACGAAAA 180
Qy 181 GAGGTCCCGGCGCAGAGGCGCTTCGCGGCGCGGAGAGAGCGCCCGCGCGG 240
Db 181 GAGGTCCCGGCGCAGAGGCGCTTCGCGGCGCGGAGAGAGCGCCCGCGCGG 240

Qy 241 GTCCGATGCGGCGCGGCTTCAAGGCTGAAATGATGCTGAGATGCGGCGCAGGCGG 300
Db 241 GTCCGATGCGGCGCGGCTTCAAGGCTGAAATGATGCTGAGATGCGGCGCAGGCGG 300
Qy 301 CGGAGAGCGGCTTGAATTTCACTTCCGCAATGCTTTTCCGCAACCCATGGAACAG 360
Db 301 CGGAGAGCGGCTTGAATTTCACTTCCGCAATGCTTTTCCGCAACCCATGGAACAG 360
Qy 361 AGTGGCCCGGAGAGGCTTCCAGAGATGCGGCGGCTTCCGCGGCGGCTTCCGCGG 420
Db 361 AGTGGCCCGGAGAGGCTTCCAGAGATGCGGCGGCTTCCGCGGCGGCTTCCGCGG 420
Qy 421 TGAAGAGTTCACTGTGTCCGCAACACTGACTATCCGATGCTGCTGCGACAC 480
Db 421 TGAAGAGTTCACTGTGTCCGCAACACTGACTATCCGATGCTGCTGCGACAC 480
Qy 481 GCCAATGCGAGCTCTCATAGCTCTGTCTCCAGAGCTTTCCCTGATGATGATCA 540
Db 481 GCCAATGCGAGCTCTCATAGCTCTGTCTCCAGAGCTTTCCCTGATGATGATCA 540
Qy 541 CGCAGTCTTCTGCTCCGCTGTTTGGCTCAGCTCCCTCAGAGGCGGCTTAAGCCC 600
Db 541 CGCAGTCTTCTGCTCCGCTGTTTGGCTCAGCTCCCTCAGAGGCGGCTTAAGCCC 600
Qy 601 AGCTGCGGCCCTTCTTCAAGTCAATGCTCTCTCCCTAGAGGATGTTCCAGCAGAGTG 660
Db 601 AGCTGCGGCCCTTCTTCAAGTCAATGCTCTCTCCCTAGAGGATGTTCCAGCAGAGTG 660
Qy 661 GCCAGTTCATTTGGGGGCTGATTTGTTGCTGAGAGAGCGGCTTACATGTTTGT 720
Db 661 GCCAGTTCATTTGGGGGCTGATTTGTTGCTGAGAGAGCGGCTTACATGTTTGT 720
Qy 721 TTCTGTAGAAAATAAACTGAGCTACGAAAA 752
Db 721 TTCTGTAGAAAATAAACTGAGCTACGAAAA 752

RESULT 3

US-08-937-263B-1/c
; Sequence 1, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng, Scanlan, Matthew,
; APPLICANT: Gure, Ali, Old, Lloyd J., Jager, Blake,
; APPLICANT: Alexander, Knuth, Drifflough, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Simm, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000

TELEFAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 752 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-937-263B-1

Query Match 4.1%; Score 30.6; DB 1; Length 752;
 Best Local Similarity 45.6%; Pred. No. 1.6;
 Matches 108; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

QY 3 CCTGTGGGCGCCCTGACCTTCTCTGAGAGCGCGGCAGAGGCTCCGAGCCATGCAAGCC 62
 DB 239 CCGCGGGGCGCCTCTCTCCCGGCGCCGAGCGCCTTGTCTCCCTGCGCCCGGAGCCTCT 180
 QY 63 GAAGCGCGGGGACAGAGGGGTTTCAGCGGCGATGCTGATGCGCCAGAGGCGCTGGCATT 122
 DB 179 GCCCGCGGTGGACACCGGCTCTCTCGGGCGCGCAGCATTTGCCCTGGGCGCATGAGAT 120
 QY 123 CCTGATGCGCCAGAGGGGCAATGCTGGCGCCAGAGAGGGGTTGCCAGCGGCGGCA 182
 DB 119 GCCAGGGGCTCTCTGGGCGCATGAGCATGCCCGTCGAAACCCCTGTGCCCCGCTTCCGC 60
 QY 183 GGTCCCCGGGCGCAGAGGGGCGCAAGAGGCGCTCGGGGCGGGAGAGGCGCCCGCG 239
 DB 59 CTGCATGGCTCCGAGGCTCTGCGCGGCTCTCAGAGAGAAAGTCAAGGCGCCACGAG 3

RESULT 4

US-08-725-182C-1/c
 Sequence 1, Application US/08725182C
 Patent No. 5804381

GENERAL INFORMATION:

APPLICANT: Yao-Tseng Chen, Scanlan, Matthew, Gure, Ali,
 APPLICANT: Old, Lloyd

TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE ENCODING
 TITLE OF INVENTION: AN ESOPHAGEAL CANCER ASSOCIATED ANTIGEN, THE ANTIGEN ITSELF,
 TITLE OF INVENTION: AND USES THEREOF

NUMBER OF SEQUENCES: 1

CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Felfe & Lynch
 STREET: 805 Third Avenue
 CITY: New York City

STATE: New York
 COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage

COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/725,182C
 FILING DATE: 03-October-1996

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. 5804381man D.

REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5466

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:

LENGTH: 752 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

US-08-725-182C-1

Query Match 4.1%; Score 30.6; DB 2; Length 752;

Best Local Similarity 45.6%; Pred. No. 1.6;
 Matches 108; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

QY 3 CCTGTGGGCGCCCTGACCTTCTCTGAGAGCGCGGCAGAGGCTCCGAGCCATGCAAGCC 62
 DB 239 CCGCGGGGCGCCTCTCTCCCGGCGCCGAGGCGCCTTGTGCTGCGCCCGGAGCCTCT 180
 QY 63 GAAGCGCGGGGACAGAGGGGTTTCAGCGGCGATGCTGATGCGCCAGAGGCGCTGGCATT 122
 DB 179 GCCCGCGGTGGACACCGGCTCTCTCGGGCGCGCAGCATTTGCCCTGGGCGCATGAGAT 120
 QY 123 CCTGATGCGCCAGAGGGGCAATGCTGGCGCCAGAGAGGCGGTTGCCAGCGGCGGCA 182
 DB 119 GCCAGGGGCTCTCTGGGCGCATGAGCATGCCCGTCGAAACCCCTGTGCCCCGCTTCCGC 60
 QY 183 GGTCCCCGGGCGCAGAGGGGCGCAAGAGGCGCTCGGGGCGGGAGAGAGCGCCCGCG 239
 DB 59 CTGCATGGCTCCGAGGCTCTGCGCGGCTCTCAGAGAGAAAGTCAAGGCGCCACGAG 3

RESULT 5

US-08-937-263B-3/c
 Sequence 3, Application US/08937263B
 Patent No. 6274145

GENERAL INFORMATION:

APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
 APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Blake;

APPLICANT: Alexander, Knuth; Drifhout, Jan W.
 TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE

TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
 TITLE OF INVENTION: ITSELF, AND USES THEREOF

NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Fulbright & Jaworski, L.L.P.
 STREET: 666 Fifth Avenue

CITY: New York City
 STATE: New York

COUNTRY: USA
 ZIP: 10103

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/937,263B
 FILING DATE: September 15, 1997

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/725,182

FILING DATE: October 3, 1996

ATTORNEY/AGENT INFORMATION:
 NAME: Sinn, Eric, Patent Agent

REGISTRATION NUMBER: 40,177
 REFERENCE/DOCKET NUMBER: LUD 5466.1

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3000

TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:

LENGTH: 32 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

US-08-937-263B-3

Query Match 3.1%; Score 23.6; DB 1; Length 32;
 Best Local Similarity 86.7%; Pred. No. 40;
 Matches 26; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 580 CAGGCGAGGCGCTAAGCCCAAGCTTGGCG 609
 DB 32 CAGGCGAGAGCGCTTAAGCCCAAGCTTGTG 3

RESULT 6
US-08-937-263B-2
; Sequence 2, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Simm, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-937-263B-2
Query Match 2.7%; Score 20.2; DB 1; Length 31;
Best Local Similarity 88.0%; Pred. No. 43;
Matches 22; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 265 GGCTGATGATGCTGCGATCGCG 289
DB 7 GGATCCATGATGCTGCGATCGCG 31
RESULT 7
US-08-937-263B-3
; Sequence 3, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA

ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Simm, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-937-263B-3
Query Match 1.7%; Score 12.6; DB 1; Length 32;
Best Local Similarity 66.7%; Pred. No. 43;
Matches 18; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
QY 591 CGTAAAGCCAGCCTGGCGCCCTTCC 617
DB 3 CACAAAGCTTGCTTAAGCGCCTTGCC 29
RESULT 8
US-08-937-263B-2/c
; Sequence 2, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drijfhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Simm, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958


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; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-937-263B-2

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SEQUENCE CHARACTERISTICS:

LENGTH: 31 base pairs
TYPE: nucleic acid

STRANDEDNESS: single

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; TOPOLOGY: linear

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US-08-937-263B-2

US-08-937-263B-2

Query Match	Score	ID	DB	Length
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Best Local Similarity	58	61	58	46

Best Local Similarity 61.5%; Pred. No. 46;
Matches 16; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 10; Indels

337 CTTTCGCACACCCATGGAAGCAGAG 362

Db 28 CATCTGCAGCATCCATGGATCCTGTG 3

Search completed: July 21, 2004, 11:14:28
Job time : 8 secs

Job time : 8 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 19, 2004, 11:55:40 ; Search time 68.5 Seconds
(without alignments)
4454.764 Million cell updates/sec

Title: US-10-023-182-1_COPY_54_593
Perfect score: 180
Sequence: 1 ATGCAGGCCGCAAGCGCGCGG.....CTCCCTCAGGCGAGAGCGCG 540

Scoring table: OLIGO
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1586107 seqs, 282547505 residues

Word size: 1

Total number of hits satisfying chosen parameters: 1192384

Minimum DB seq length: 5

Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Command line parameters:

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-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=45 -MODE=LOCAL
-OUTMT=dplo -NORM=ext -HEAPSIZE=500 -MINLEN=5 -MAXLEN=50
-USER=US10023182_0CGN 1.1.155_@runat_19072004_125307_4267 -NCPU=6 -ICPU=3
-NO_WMAP -LARGESQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOC
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

1: Geneseq_29Jan04:*
2: Geneseqp1980s:*
3: Geneseqp1990s:*
4: Geneseqp2000s:*
5: Geneseqp2001s:*
6: Geneseqp2002s:*
7: Geneseqp2003as:*
8: Geneseqp2003bs:*
8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	16.7	30	5	AAU85104 Human NTN
2	30	16.7	30	5	AAU85111 Human NTN
3	30	16.7	30	5	AAU85108 Human NTN
4	30	16.7	30	5	AAU85109 Human NTN
5	30	16.7	30	5	AAU85119 Human LAG
6	30	16.7	30	5	AAU85105 Human NTN
7	30	16.7	30	5	AAU85116 Human NTN
8	30	16.7	30	5	AAU85110 Human NTN
9	30	16.7	30	5	AAU85106 Human NTN
10	30	16.7	30	5	AAU85103 Human NTN

11	30	16.7	30	5	AAU85115 Human NTN
12	30	16.7	30	5	AAU85107 Human NTN
13	30	16.7	30	5	AAU85112 Human NTN
14	30	16.7	30	7	ADD35566 Human NY-
15	29	16.1	30	5	AAU85127 Human LAG
16	29	16.1	30	5	AAU85114 Human NTN
17	28	15.6	28	6	ABP74370 Human NY-
18	28	15.6	28	6	ABP74371 Human NY-
19	28	15.6	28	7	ADC09230 Epitope w
20	28	15.6	28	7	ADC09229 Epitope w
21	28	15.6	30	5	AAU85120 Human LAG
22	28	15.6	30	5	AAU85102 Human NTN
23	27	15.0	27	4	AAE07757 Human HLA
24	27	15.0	27	4	AAE07717 Human NY
25	25	13.9	25	7	ADD71521 HLA-DP4 b
26	25	13.9	25	7	ADD71522 HLA-DP4 b
27	25	13.9	25	7	ADD71532 HLA-DP4 b
28	25	13.9	30	5	AAU85128 Human LAG
29	23	12.8	23	7	ADD71520 HLA-DP4 b
30	23	12.2	30	5	AAU85118 Human LAG
31	22	11.7	21	7	ADD71449 Human NY
32	21	11.1	20	2	AAV05979 Human can
33	20	11.1	20	2	AAE07744 Human ESO
34	20	11.1	20	4	AAE07746 Human ESO
35	20	11.1	20	4	AAE07743 Human ESO
36	20	11.1	20	4	AAE07731 Human NY
37	20	11.1	20	4	AAE07729 Human NY
38	20	11.1	20	4	AAE07742 Human ESO
39	20	11.1	20	4	AAE07747 Human ESO
40	20	11.1	20	4	AAE07732 Human NY
41	20	11.1	20	4	AAE07745 Human ESO
42	20	11.1	20	4	AAE07744 Human ESO
43	20	11.1	20	7	ADD71448 Human tum
44	20	11.1	18	3	AAV52435 Human tum
45	18	10.0	18	3	AAV52435 Human tum

ALIGNMENTS

RESULT 1	AAU85104 standard; peptide; 30 AA.
AAU85104	
ID	AAU85104; (first entry)
AC	08-MAY-2002 . (first entry)
AC	AAU85104;
XX	
DT	Human MYNSOLA segment 3.
XX	
DE	
XX	
XX	Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW	viral infection; human immunodeficiency virus; melanoma;
KW	bacterial infection; Salmonella; Legionella; paratubercular infection;
KW	Trypanosoma; Toxoplasma; Giardia.
XX	
OS	Homo sapiens.
XX	
PN	WO200190197-A1.
XX	
PD	29-NOV-2001.
XX	
PF	25-MAY-2001; 2001WO-AU000622.
XX	
PR	26-MAY-2000; 2000AU-00007761.
XX	
PA	(AUSU) UNIV AUSTRALIAN NAT.
XX	
PI	Thomson SA, Ramshaw JA;
XX	
DR	WPI: 2002-147575/19.
XX	
DR	N-PSDB; ABK36924.
XX	
PT	New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the


```
XX Homo sapiens.
OS
XX WO200190197-A1.
PN
XX
XX 29-NOV-2001.
PD
XX
XX 25-MAY-2001; 2001WO-AU000622.
PF
XX 26-MAY-2000; 2000AU-00007761.
PR
XX (AUSU ) UNIV AUSTRALIAN NAT.
PA
XX Thomson SA, Ramshaw IA;
PI
XX WPI; 2002-147575/19.
DR
XX N-PSDB; ABK36928.
DR
XX
XX New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
XX Example 3; Fig 27; 364pp; English.
XX
XX The invention relates to a new synthetic polypeptide (I) comprising
XX several different segments of at least one parent polypeptide linked
XX together in a different relationship relative to their linkage in the
XX parent polypeptide to impede, abrogate or otherwise alter at least one
XX function associated with the parent polypeptide and for inducing an
XX immune response against a pathogen or cancer. Also included are a
XX synthetic polynucleotide encoding and a computer system for designing the
XX synthetic polypeptides. The synthetic polypeptides and polynucleotides
XX are referred to as a Savine. The synthetic polypeptide is useful for
XX modulating immune responses preferably directed against a pathogen or a
XX cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
XX and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
XX oesophagus, brain, testicle, uterus), as potentiating agents.
XX Compositions comprising the polypeptide may be used in the treatment or
XX prophylaxis against viral (such as infections caused by HIV (human
XX immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
XX virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
XX (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
XX Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
XX (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
XX Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
XX a peptide derived from a parent protein used to construct a savine of the
XX invention
XX
XX SQ Sequence 30 AA;
XX
XX Alignment Scores:
XX Pred. No.: 8.46e-19 Length: 30
XX Score: 30.00 Matches: 30
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 16.67% Indels: 0
XX DB: 5 Gaps: 0
XX
XX US-10-023-182-1_COPY_54_593 (1-540) x AAU85109 (1-30)
XX
XX 265 GAGTTCCTGCGGACGCTTGGGACACCCAGTGAAGAGAGAGCTGGCCGCGAGAGC 324
XX |||||||
XX Db 1 GlnPheTryLeuAlaMetCProPheAlaThrProMetGlnAlaGlnLeuAlaArgArgSer 20
XX |||||||
XX 325 CTGGCCCGAGATCCCAACCGCTTCCCGTG 354
XX |||||||
XX Db 21 LeuAlaGlnAlaPalaProProleuProval 30
XX |||||||
XX
XX RESULT 4
XX AAU85109
XX ID AAU85109 standard; peptide; 30 AA.
XX
```

```
AC AAU85109;
XX
XX 08-MAY-2002 (first entry)
DT
XX
XX Human NYSNOLA segment 8.
DE
XX
XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficiency virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
XX
XX Homo sapiens.
OS
XX WO200190197-A1.
PN
XX
XX 29-NOV-2001.
PD
XX
XX 25-MAY-2001; 2001WO-AU000622.
PF
XX 26-MAY-2000; 2000AU-00007761.
PR
XX (AUSU ) UNIV AUSTRALIAN NAT.
PA
XX Thomson SA, Ramshaw IA;
PI
XX WPI; 2002-147575/19.
DR
XX N-PSDB; ABK36929.
DR
XX
XX New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
XX Example 3; Fig 27; 364pp; English.
XX
XX The invention relates to a new synthetic polypeptide (I) comprising
XX several different segments of at least one parent polypeptide linked
XX together in a different relationship relative to their linkage in the
XX parent polypeptide to impede, abrogate or otherwise alter at least one
XX function associated with the parent polypeptide and for inducing an
XX immune response against a pathogen or cancer. Also included are a
XX synthetic polynucleotide encoding and a computer system for designing the
XX synthetic polynucleotides. The synthetic polypeptides and polynucleotides
XX are referred to as a Savine. The synthetic polypeptide is useful for
XX modulating immune responses preferably directed against a pathogen or a
XX cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
XX and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
XX oesophagus, brain, testicle, uterus), as potentiating agents.
XX Compositions comprising the polypeptide may be used in the treatment or
XX prophylaxis against viral (such as infections caused by HIV (human
XX immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
XX virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
XX (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
XX Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
XX (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
XX Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
XX a peptide derived from a parent protein used to construct a savine of the
XX invention
XX
XX SQ Sequence 30 AA;
XX
XX Alignment Scores:
XX Pred. No.: 8.46e-19 Length: 30
XX Score: 30.00 Matches: 30
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 16.67% Indels: 0
XX DB: 5 Gaps: 0
XX
XX US-10-023-182-1_COPY_54_593 (1-540) x AAU85109 (1-30)
XX
XX 310 CTGGCCCGAGAGAGCTGGCCGAGATGCCACCGCTTCCCGTGCGAGGGGTCTTCTG 369
XX |||||||
XX
```


CC Salmoneila, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
SQ Sequence 30 AA;
Alignment Scores:
Pred. No.: 8,46e-19 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x AAU85105 (1-30)
QY 130 GGTCCCGGGGGCGAGGGGCGAGGCGCTCGGGGCGGAGAGGCGCCCGCGGGGT 189
Db 1 GlyProArGlyAlaGlyAlaAlaArgAlaSerGlyProGlyGlyAlaProArgGly 20
QY 190 CCGCATGGCGGCGCGGCTTCAGGGCTGAAT 219
Db 21 ProHisGlyGlyAlaAlaAlaSerGlyLeuAsn 30
RESULT 7
AAU85116
ID AAU85116 standard; peptide: 30 AA.
XX
AC AAU85116;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human NYNSOLb segment 3.
XX
KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficiency virus; melanoma;
KW bacterial infection; Salmoneila; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
XX
OS Homo sapiens.
XX
PN WO200190197-A1.
XX
PD 29-NOV-2001.
XX
XX 25-MAY-2001; 2001WO-AU000622.
XX
PR 26-MAY-2000; 2000AU-00007761.
XX
PA (AUSU) UNIV AUSTRALIAN NAT.
XX
PI Thomson SA, Ramshaw IA;
XX
DR WPI: 2002-147575/19.
XX
N-PSDB; ABK36936.
XX
PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
PS Example 3; Fig 27; 364pp; English.
XX
CC The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides

CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus); as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmoneila, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
SQ Sequence 30 AA;
Alignment Scores:
Pred. No.: 8,46e-19 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x AAU85116 (1-30)
QY 125 GCAAGGTCCCGGGCGCGAGGGCGAGGCGCTCGGGGCGGAGAGGCGCCCGCG 184
Db 1 AlaGluVal1ProGlyAlaGlnGlyGlnGlyProArgGlyArgGluGluAlaProArg 20
QY 185 GGGTCCGCATGGCGGCGCGGCTTCAGGGC 214
Db 21 GlyValAlaGluMetAlaAlaArgLeuGlnGly 30
RESULT 8
AAU85110
ID AAU85110 standard; peptide: 30 AA.
XX
AC AAU85110;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human NYNSOLA segment 9.
XX
KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficiency virus; melanoma;
KW bacterial infection; Salmoneila; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
XX
OS Homo sapiens.
XX
PN WO200190197-A1.
XX
PD 29-NOV-2001.
XX
XX 25-MAY-2001; 2001WO-AU000622.
XX
PR 26-MAY-2000; 2000AU-00007761.
XX
PA (AUSU) UNIV AUSTRALIAN NAT.
XX
PI Thomson SA, Ramshaw IA;
XX
DR WPI: 2002-147575/19.
XX
N-PSDB; ABK36930.
XX
PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX

PS Example 3; Fig 27; 364pp; English.
XX
XX The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
SQ Sequence 30 AA;

Alignment Scores:
Pred. No.: 8,466-19 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 5 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x AAU85110 (1-30)

QY 355 CCAGGGGTCCTCTGTAAGAGTTCACCTGTCGCGACATCTGATCCGACTGACT 414
DB 1 PGGlyValIleuLeuLysGIuPheThrValSerGIyAAsIleuThrIleArgLeuThr 20
QY 415 GCTGCAGACCAACCCCACTGACGCTCTCC 444
DB 21 AAlaAlaSPHisArgGIuLeuGIuLeuSer 30

RESULT 9
AAU85106
ID AAU85106 standard; peptide; 30 AA.
XX
XX AAU85106;
AC
XX
XX 08-MAY-2002 (first entry)
DT
XX
XX Human NYNSOLA segment 5.
DE
XX
XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KM viral infection; human immunodeficiency virus; melanoma;
KM bacterial infection; Salmonella; Legionella; parasitic infection;
KM Trypanosoma; Toxoplasma; Giardia.
XX
XX Homo sapiens.
OS
XX
XX WO200190197-A1.
PN
XX
XX 29-NOV-2001.
PD
XX
XX 25-MAY-2001; 2001WO-AU000622.
PF
XX
XX 26-MAY-2000; 2000AU-00007761.
PR
XX
XX (AUSU) UNIV AUSTRALIAN NAT.
PA
XX

PI Thomson SA; Ramshaw IA;
XX
XX WPI; 2002-147575/19.
DR
XX N-PsDB; ABK36926.
DR
XX
XX New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
XX
PS Example 3; Fig 27; 364pp; English.
XX
XX The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
XX
SQ Sequence 30 AA;

Alignment Scores:
Pred. No.: 8,466-19 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 5 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x AAU85106 (1-30)

QY 175 GAGCGCCCGCGGGTCCGATGCGCGCGCTTCAGGCTGAATGCATGCTGCAGATGC 234
DB 1 GIyAlaPProAlArgGIyProHIEGIyGIyAlaAlaSerGIyLeuAanGIyCySCyAlaGIyS 20
QY 235 GGGCGCAGGGGGCGGAGAGCGGCTGCTT 264
DB 21 GIyAlaArgGIyProGIuSerArgIuLeu 30

RESULT 10
AAU85103
ID AAU85103 standard; peptide; 30 AA.
XX
XX AAU85103;
AC
XX
XX 08-MAY-2002 (first entry)
DT
XX
XX Human NYNSOLA segment 2.
DE
XX
XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KM viral infection; human immunodeficiency virus; melanoma;
KM bacterial infection; Salmonella; Legionella; parasitic infection;
KM Trypanosoma; Toxoplasma; Giardia.
XX
XX Homo sapiens.
OS
XX


```
PN WO200190197-A1.
XX
XX 29-NOV-2001.
XX
XX 25-MAY-2001; 2001WO-AU000622.
XX
XX 26-MAY-2000; 2000AU-00007761.
XX
XX (AUSU ) UNIV AUSTRALIAN NAT.
XX
XX Thomson SA, Ramshaw IA;
XX
XX MPI, 2002-147575/19.
XX
XX N-PSDB; ABK36923.
XX
XX New synthetic polypeptides having several different segments of at least
XX one parent polypeptide linked together differently compared to the
XX linkage in the parent polypeptide, for inducing immune response against a
XX pathogen or cancer.
XX
XX Example 3; Fig 27; 364pp; English.
XX
XX The invention relates to a new synthetic polypeptide (I) comprising
XX several different segments of at least one parent polypeptide linked
XX together in a different relationship relative to their linkage in the
XX parent polypeptide to impede, abrogate or otherwise alter at least one
XX function associated with the parent polypeptide and for inducing an
XX immune response against a pathogen or cancer. Also included are a
XX synthetic polynucleotide encoding and a computer system for designing the
XX synthetic polypeptides. The synthetic polypeptides and polynucleotides
XX are referred to as a Savine. The synthetic polypeptide is useful for
XX modulating immune responses preferably directed against a pathogen or a
XX cancer. (e.g., cancers of the lung, breast, ovary, cervix, colon, head
XX and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
XX oesophagus, brain, testicle, uterus), as potentiating agents.
XX Compositions comprising the polypeptide may be used in the treatment or
XX prophylaxis against viral (such as infections caused by HIV (human
XX immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
XX virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
XX (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
XX Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
XX (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
XX Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
XX a peptide derived from a parent protein used to construct a savine of the
XX invention
XX
XX Sequence 30 AA;
XX
XX Alignment Scores:
XX Pred. No.: 8,46e-19 Length: 30
XX Score: 30.00 Matches: 30
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 16.67% Indels: 0
XX DB: Gaps: 0
XX
XX US-10-023-182-1_copy_54_593 (1-540) x AAU85103 (1-30)
XX
XX 40 GATGCTGATGCGCCGAGAGGCGCTTCTGATGCGCCGAGGCGGCAATGCTGCGCGC 99
XX
XX 1 AapalaaapglpProgllylIleProaapglpProgllylYAsnlaaglygly 20
XX
XX 100 CCAGAGAGGCGGCGGCGCCAGCGGCGGCGAGA 129
XX
XX 21 ProgllylualaaGlyAlaThrIglylYArg 30
XX
XX RESULT 11
XX AAU85115
XX ID AAU85115 standard; peptide; 30 AA.
XX AC AAU85115;
XX XX
XX DT 08-MAY-2002 (first entry)
```

```
XX
XX Human NYNSO1b segment 2.
XX
XX DE
XX XX
XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
XX viral infection; human immunodeficiency virus; melanoma;
XX bacterial infection; Salmonella; Legionella; parasitic infection;
XX Trypanosoma; Toxoplasma; Giardia.
XX
XX OS
XX Homo sapiens.
XX
XX PN WO200190197-A1.
XX
XX 29-NOV-2001.
XX
XX 25-MAY-2001; 2001WO-AU000622.
XX
XX 26-MAY-2000; 2000AU-00007761.
XX
XX (AUSU ) UNIV AUSTRALIAN NAT.
XX
XX Thomson SA, Ramshaw IA;
XX
XX MPI, 2002-147575/19.
XX
XX N-PSDB; ABK36935.
XX
XX New synthetic polypeptides having several different segments of at least
XX one parent polypeptide linked together differently compared to the
XX linkage in the parent polypeptide, for inducing immune response against a
XX pathogen or cancer.
XX
XX Example 3; Fig 27; 364pp; English.
XX
XX The invention relates to a new synthetic polypeptide (I) comprising
XX several different segments of at least one parent polypeptide linked
XX together in a different relationship relative to their linkage in the
XX parent polypeptide to impede, abrogate or otherwise alter at least one
XX function associated with the parent polypeptide and for inducing an
XX immune response against a pathogen or cancer. Also included are a
XX synthetic polynucleotide encoding and a computer system for designing the
XX synthetic polypeptides. The synthetic polypeptides and polynucleotides
XX are referred to as a Savine. The synthetic polypeptide is useful for
XX modulating immune responses preferably directed against a pathogen or a
XX cancer. (e.g., cancers of the lung, breast, ovary, cervix, colon, head
XX and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
XX oesophagus, brain, testicle, uterus), as potentiating agents.
XX Compositions comprising the polypeptide may be used in the treatment or
XX prophylaxis against viral (such as infections caused by HIV (human
XX immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
XX virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
XX (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
XX Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
XX (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
XX Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
XX a peptide derived from a parent protein used to construct a savine of the
XX invention
XX
XX Sequence 30 AA;
XX
XX Alignment Scores:
XX Pred. No.: 8,46e-19 Length: 30
XX Score: 30.00 Matches: 30
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 16.67% Indels: 0
XX DB: Gaps: 0
XX
XX US-10-023-182-1_copy_54_593 (1-540) x AAU85115 (1-30)
XX
XX 80 CAGGCGGCAATGCTGCGGCGCCGAGAGGCGGCTTCTGATGCGGCGGCAAGAGCTCCCGGG 139
XX
XX 1 GlnGlylAwetLauAlaAlaGlnGlnIuArgYAlProARgAlaAlaGlnAlProGly 20
XX
XX 140 GCGCAGGCGCAGCAAGGCGCTCGGGCGCGG 169
```

```

Db      21  |||||
RESULT 12  21  AAlaGInGlyGInGInGlyProAlrGlyArg 30
AAU85107
ID      AAU85107 standard; peptide; 30 AA.
XX
AC      AAU85107;
XX
DT      08-MAY-2002 (first entry)
XX
DE      Human NYNSOLA segment 6.
XX
KW      Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW      viral infection; human immunodeficiency virus; melanoma;
KW      bacterial infection; Salmonella; Legionella; parasitic infection;
KW      Trypanosoma; Toxoplasma; Giardia.
XX
OS      Homo sapiens.
XX
PN      WO200190197-A1.
XX
PD      29-NOV-2001.
XX
PF      25-MAY-2001; 2001WO-AU000622.
XX
PR      26-MAY-2000; 2000AU-00007761.
XX
PA      (AUSU ) UNIV AUSTRALIAN NAT.
XX
PI      Thomson SA, Ramshaw IA;
XX
DR      WPI; 2002-147575/19.
XX
N-PSDB; ABR36932.
XX
PT      New synthetic polypeptides having several different segments of at least
PT      one parent polypeptide linked together differently compared to the
PT      linkage in the parent polypeptide, for inducing immune response against a
PT      pathogen or cancer.
XX
XX
XX      Example 3; Fig 27; 364pp; English.
XX
XX      The invention relates to a new synthetic polypeptide (I) comprising
XX      several different segments of at least one parent polypeptide linked
XX      together in a different relationship relative to their linkage in the
XX      parent polypeptide to impede, abrogate or otherwise alter at least one
XX      function associated with the parent polypeptide and for inducing an
XX      immune response against a pathogen or cancer. Also included are a
XX      synthetic polynucleotide encoding and a computer system for designing the
XX      synthetic polypeptides. The synthetic polypeptides and polynucleotides
XX      are referred to as a Savine. The synthetic polypeptide is useful for
XX      modulating immune responses preferably directed against a pathogen or a
XX      cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
XX      and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
XX      oesophagus, brain, testicle, uterus), as potentiating agents.
XX      Compositions comprising the polypeptide may be used in the treatment or
XX      prophylaxis against viral (such as infections caused by HIV (human
XX      immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
XX      virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
XX      (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
XX      Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
XX      (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
XX      Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
XX      a peptide derived from a parent protein used to construct a savine of the
XX      invention
XX
SQ      Sequence 30 AA;

```

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Query Match: 16.67% Indels: 0
DB: 5 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x AAU85107 (1-30)
OY      220  GGATCTCTGCAGATGGGGGCGGAGAGCCCTGCTTGAATTCTACTCGCC 279
DB      1    GlyCysCysArgCysGlyAlaArgGlyProGlnSerArgLeuLeuGlnPheTyrLeuAla 20
OY      280  ATGCCTTTCGACACACCATGGAAGCAGAG 309
DB      21  MetProPheAlaThrProMetGlnAlaGln 30
RESULT 13
AAU85112
ID      AAU85112 standard; peptide; 30 AA.
XX
AC      AAU85112;
XX
DT      08-MAY-2002 (first entry)
XX
DE      Human NYNSOLA segment 11.
XX
KW      Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW      viral infection; human immunodeficiency virus; melanoma;
KW      bacterial infection; Salmonella; Legionella; parasitic infection;
KW      Trypanosoma; Toxoplasma; Giardia.
XX
OS      Homo sapiens.
XX
PN      WO200190197-A1.
XX
PD      29-NOV-2001.
XX
PF      25-MAY-2001; 2001WO-AU000622.
XX
PR      26-MAY-2000; 2000AU-00007761.
XX
PA      (AUSU ) UNIV AUSTRALIAN NAT.
XX
PI      Thomson SA, Ramshaw IA;
XX
DR      WPI; 2002-147575/19.
XX
N-PSDB; ABR36932.
XX
PT      New synthetic polypeptides having several different segments of at least
PT      one parent polypeptide linked together differently compared to the
PT      linkage in the parent polypeptide, for inducing immune response against a
PT      pathogen or cancer.
XX
XX
XX      Example 3; Fig 27; 364pp; English.
XX
XX      The invention relates to a new synthetic polypeptide (I) comprising
XX      several different segments of at least one parent polypeptide linked
XX      together in a different relationship relative to their linkage in the
XX      parent polypeptide to impede, abrogate or otherwise alter at least one
XX      function associated with the parent polypeptide and for inducing an
XX      immune response against a pathogen or cancer. Also included are a
XX      synthetic polynucleotide encoding and a computer system for designing the
XX      synthetic polypeptides. The synthetic polypeptides and polynucleotides
XX      are referred to as a Savine. The synthetic polypeptide is useful for
XX      modulating immune responses preferably directed against a pathogen or a
XX      cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
XX      and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
XX      oesophagus, brain, testicle, uterus), as potentiating agents.
XX      Compositions comprising the polypeptide may be used in the treatment or
XX      prophylaxis against viral (such as infections caused by HIV (human
XX      immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
XX      virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
XX      (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
XX      Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
XX      (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
XX      Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is

```

Alignment Scores: 8.46e-19 Length: 30
 Score: 30.00 Matches: 30
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

CC	a peptide derived from a parent protein used to construct a savine of the invention		
XX	Sequence 30 AA;		
SQ	Alignment Scores:		
Pred. No.:	8.46e-19	Length:	30
Score:	30.00	Matches:	30
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	16.67%	Indels:	0
DB:	5	Gaps:	0
US-10-023-182-1_COPY_54_593 (1-540) x AAU85112 (1-30)			
OY	445 ATCAGCTCCTGTCTTCACGAGCTTTCCCTGTGATGTGATCACGAGTGCTTTCGCC 504 		
Dd	1 ILESERSrCySleuGIInIleuserrLeuMeTrIpLlEthrdIncysPheLeuPro 20 		
OY	505 GTGTTTTGGCTCAGCGCTTCCTTCAGGGCAG 534 		
Dd	21 ValPheLeuAlaGlInProPserGlycin 30 		
RESULT 14			
ADD35566	standard; peptide; 30 AA.		
ID	ADD35566 standard; peptide; 30 AA.		
XX			
AC	ADD35566;		
XX			
DT	15-JAN-2004 (first entry)		
XX			
DE	Human NY-ESO-1 peptide SEQ ID NO:16.		
XX			
KM	human leukocyte antigen; HLA; cytolytic T cell stimulator; immune response; cytosolic; gene therapy; human; NY-ESO-1; immunogenic tumour antigen.		
XX			
OS	Homo sapiens.		
XX			
PN	WO2003068800-A2.		
XX			
PD	21-AUG-2003.		
PF	12-FEB-2003; 2003WO-US004182.		
XX			
PR	13-FEB-2002; 2002US-0355828P.		
XX			
PA	(LUDW-) LUDWIG INST CANCER RES.		
XX			
PI	Jager E, Knuth A, Old L, Gnjatich S;		
XX			
DR	WPI; 2003-902684/82.		
PT	New isolated peptide that binds to an HLA molecule, useful for treating a subject with a disorder characterized by the presence of complexes of an HLA molecule and the peptide, e.g. cancer, and for inducing immune response.		
XX			
PS	Example 9; SEQ ID NO 16; 73pp; English.		
XX			
CC	The present invention describes an isolated peptide (1) consisting of 8-11, which binds to a human leukocyte (HLA) molecule, e.g. an HLA-A3, HLA-B35 or an HLA-B51 molecule, and stimulates cytolytic T cells specific for complexes of the peptide and the HLA molecule, where at least 8 contiguous amino acids of the peptide consist of at least 8 contiguous amino acid sequence of p94-102, p93-101, p108-116 or p91-99. Also described: (1) a composition comprising (1) and a carrier; (2) an isolated nucleic acid molecule encoding (1) or the polypeptide; (3) an expression vector comprising the nucleic acid of (2) in operable linkage with a promoter; (4) a host cell transformed with the nucleic acid of (2) or the expression vector of (3); (5) an isolated cytolytic T-cell (CTL) specific for a complex of the HLA molecule and (1); (6) detecting the CTL of (5); (7) a polytope comprising at least two of (1) that are linked		

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CC together; (8) an isolated nucleic acid that encodes the polypeptide; (9) an
CC isolated tetramer comprising the HLA molecule, biotin and a carrier; (11)
CC partner; (10) a composition comprising the tetramer and a carrier; (11)
CC inducing an immune response in a subject; (12) treating a subject with a
CC disorder characterised by the presence of complexes of an HLA molecule
CC and the peptide; (13) a combinatorial library of derivatives of (1),
CC where the derivatives consist of 8-11 amino acids; (14) a screening assay
CC for an analogue of (1); (15) an isolated antibody or its fragment that
CC specifically binds a HLA/peptide complex, or (1); (16) an isolated
CC soluble T cell receptor that specifically binds to a HLA/peptide complex;
CC and (17) inducing an immune response on a subject having a disorder
CC characterised by the presence of the HLA molecule and the peptide. (1)
CC has cytostatic activity, and can be used in gene therapy. The peptides,
CC nucleic acid molecules, vectors, compositions, antibodies and methods are
CC useful for treating a subject with a disorder characterised by the
CC presence of complexes of an HLA molecule and the peptide, and for
CC inducing an immune response. The present sequence represents a human NY-
CC ESO-1 peptide, which is used in the exemplification of the present
CC invention. NY-ESO-1 is an immunogenic tumour antigen.
XX
XX Sequence 30 AA;
SQ
Alignment Scores:
Pred. No.: 8,46e-19 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x ABD35566 (1-30)
QY 238 GCCAGGGGCGCGAGAGCGCGCTGTGATCTTACCTGCGCCATGCGCTTTCGACACCC 297
Db 1 AAlaArgGjProGluSerfArgIeuLeuGluPheTyRleuAlaMetCProPheAlaThrPro 20
QY 298 ATGGAAGCAGAGCTGGCGCGCAGAGCCTG 327
Db 21 MetGluAlaGluLeuAlaArgfArgSerLeu 30
RESULT 15
ID AAU85127 standard; peptide; 30 AA.
XX AAU85127;
XX AC
XX 08-MAY-2002 (first entry)
XX DE
XX Human LAGE1 segment 10.
XX KM
XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
XX KM viral infection; human immunodeficiency virus; melanoma;
XX KM bacterial infection; Salmonella; Legionella; parasitic infection;
XX KM Trypanosoma; Toxoplasma; Giardia.
XX OS
XX Homo sapiens.
XX PN
XX WO200190197-A1.
XX XX
XX 29-NOV-2001.
XX PD
XX 25-MAY-2001; 2001WO-AU000622.
XX PF
XX 26-MAY-2000; 2000AU-00007761.
XX PR
XX (AUSU ) UNIV AUSTRALIAN NAT.
XX PA
XX Thomson SA, Ramshaw IA;
XX PI
XX WPI; 2002-147575/19.
XX DR
XX N-PSDB; ABK36947.
XX
XX New synthetic polypeptides having several different segments of at least

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PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
XX pathogen or cancer.

PS Example 3; Fig 27; 364pp; English.

XX The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer. (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention

XX Sequence 30 AA;

SO Alignment Scores:

Pred. No.: 7.18e-18 Length: 30
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.11% Indels: 0
DB: 5 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x AAU85127 (1-30)

OY 403 ATCCGACGTGACGCTGCGACACGACCGCCACGTGACGCTTCATCATGCTCTGCTCCAG 462
DB 2 IleaArgLeuThrAlaAlaAspHisArgGlnLeuGlnLeuSerHisSerSerCysLeuGln 21

OY 463 CAGCTTCCCTGCTGATGTCGATCCAG 489
DB 22 GlnLeuSerLeuMetMetTrpIleThr 30

RESULT 16

AAU85114

AC AAU85114 standard; peptide; 30 AA.

DT 08-MAY-2002 (first entry)

DE Human NYNSO1b segment 1.

KM Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KM viral infection; human immunodeficiency virus; melanoma;
KM bacterial infection; Salmonella; Legionella; parasitic infection;
KM Trypanosoma; Toxoplasma; Giardia.

OS Homo sapiens.

PN WO200190197-A1.

PD 29-NOV-2001.

PF 25-MAY-2001; 2001WO-AU000622.

PR 26-MAY-2000; 2000AU-00007761.

XX (AUSU) UNIV AUSTRALIAN NAT.

PI Thomson SA, Ramshaw JA;

DR WPI; 2002-147575/19.

DR N-PSDB; ABR36934.

PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.

PS Example 3; Fig 27; 364pp; English.

XX The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer. (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention

XX Sequence 30 AA;

SO Alignment Scores:

Pred. No.: 7.18e-18 Length: 30
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.11% Indels: 0
DB: 5 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x AAU85114 (1-30)

OY 38 GCGATGCTGATGGCCGACGAGCGCCGATTCGATGCGCCAGGGGCAATGCTGGCG 97
DB 2 AlaMetLeuMetAlaGlnGlnAlaLeuAlaPheLeuMetAlaGlnGlnAlaMetLeuAla 21

OY 98 GCCCAGAGAGCGCGGTGCCACGGGCG 124
DB 22 AlaGlnGlnAlaArgValProArgAla 30

RESULT 17

ABP74370

ID ABP74370 standard; peptide; 28 AA.

AC ABP74370;

DT 03-FEB-2003 (first entry)

DE Human NY-ESO-1 epitope SEQ ID NO:254.

KM Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
T cell.

XX	Unidentified.
XX	WO2003008537-A2.
XX	30-JAN-2003.
XX	29-MAR-2002; 2002WO-US010189.
XX	06-APR-2001; 2001US-028221IP.
XX	PR 07-NOV-2001; 2001US-0337017P.
XX	PR 07-MAR-2002; 2002US-0363210P.
XX	(CTL1-) CTL IMMUNOTHERAPIES CORP.
XX	Simard JYL, Diamond DC, Liu L, Xie Z;
XX	WPI; 2003-248010/24.
XX	Epitope having high affinity for major histocompatibility complex class I
XX	PT useful for treating an animal, evaluating immunogenicity of a vaccine or
XX	therapeutic composition and for diagnosing a disease.
XX	Claim 1; SEQ ID NO 255; 239pp; English.
XX	The invention relates to an isolated epitope polypeptide that has high
CC	affinity for major histocompatibility complex (MHC) class I, and an
CC	epitope cluster comprising the polypeptide. Also disclosed is a vaccine
CC	or immunotherapeutic composition containing an epitope of the invention.
CC	Compositions of the invention may be used in the treatment of cancer. The
CC	method can be combined with a radiation therapy, chemotherapy,
CC	biochemotherapy or surgery. The composition is also useful for evaluating
CC	immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC
CC	-peptide complexes of the invention are useful for determining specific T
CC	cell frequency. This method is useful for evaluating immunological
CC	response by performing the method prior to and subsequent to an
CC	immunisation step. Compositions of the invention are useful for
CC	diagnosing a disease. The current sequence represents an epitope of the
CC	invention with high affinity for MHC class I.
XX	Sequence 28 AA:
SO	
Alignment Scores:	
Pred. No.:	6.16e-17 Length: 28
Score:	28.00 Matches: 28
Percent Similarity:	100.00% Conservative: 0
Best local Similarity:	100.00% Mismatches: 0
Query Match:	15.56% Indels: 0
DB:	7 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x ADC09230 (1-28)	
QY	448 AGTCTCCGTCCTCAGACGCTTTCCCTGTGAATGGAAACAGCAAGTGCTTTCGCCCGTG 507
Db	1 SerSetcysIeuIndInIeusSerIeuEueMetPrlleThrGlnCySPheLeuProVal 20
QY	508 TTTTTGGACTCAGCGCTCCCTCAGAG 531
Db	21 PheLeuAlaGlnProProSergly 28
RESULT 20	
ADC09229	
ID	ADC09229 standard; peptide; 28 AA.
XX	
AC	ADC09229;
XX	
DT	18-DEC-2003 (first entry)
DE	
XX	
XX	Epitope with high affinity for MHC class I #SEQ ID 254.
KM	Epitope; immunological; vaccine;
KM	major histocompatibility complex class I; MHC class I; cancer;
KM	immunisation.

XX Unidentified.
 XX
 XX W02003008537-A2.
 XX
 XX 30-JAN-2003.
 XX
 XX
 XX 29-MAR-2002; 2002WO-US010189.
 XX
 XX 06-APR-2001; 2001US-0282211P.
 XX 07-NOV-2001; 2001US-0337017P.
 XX 07-MAR-2002; 2002US-0363210P.
 XX
 XX (CTL1-) CTL IMMUNOTHERAPIES CORP.
 XX
 XX Simard JTL, Diamond DC, Liu L, Xie Z;
 XX WPI; 2003-248010/24.
 XX
 XX Epitope having high affinity for major histocompatibility complex class I
 XX useful for treating an animal, evaluating immunogenicity of a vaccine or
 XX therapeutic composition and for diagnosing a disease.
 XX
 XX Claim 1; SEQ ID NO 254; 239pp; English.
 XX
 XX The invention relates to an isolated epitope polypeptide that has high
 XX affinity for major histocompatibility complex (MHC) class I, and an
 XX epitope cluster comprising the polypeptide. Also disclosed is a vaccine
 XX or immunotherapeutic composition containing an epitope of the invention.
 XX Compositions of the invention may be used in the treatment of cancer. The
 XX method can be combined with a radiation therapy, chemotherapy,
 XX biochemotherapy or surgery. The composition is also useful for evaluating
 XX immunogenicity of a vaccine or immunotherapeutic compound. Multimeric MHC
 XX -peptide complexes of the invention are useful for determining specific T
 XX cell frequency. This method is useful for evaluating immunological
 XX response, by performing the method prior to and subsequent to an
 XX immunisation step. Compositions of the invention are useful for
 XX diagnosing a disease. The current sequence represents an epitope of the
 XX invention with high affinity for MHC class I.
 XX
 XX Sequence 28 AA:
 XX
 XX Alignment Scores:
 XX Pred. No: 6.16e-17 Length: 28
 XX Score: 28.00 Matches: 28
 XX Percent Similarity: 100.00% Conserved: 0
 XX Best Local Similarity: 100.00% Mismatches: 0
 XX Query Match: 15.56% Indels: 0
 XX DB: 7 Gaps: 0
 XX
 XX US-10-023-182-1_COPY_54_593 (1-540) x ADC09229 (1-28)
 QY 406 CGACGTACGTCGCGACACCGCAACTGACGCTCTCATCAGCTCTGCTCCAGCAG 465
 Db 1 ArguenhrhAlaAlaSpHsArgGlnuEnglnuEnuSerIleSerCySleuGlnGln 20
 QY 466 CTTTCCTGTTGATGTCGATCAGC 489
 Db 21 leuSerleuMetTrpIleThr 28
 RESULT 21
 ID AAU85120
 AC AAU85120 standard; peptide; 30 AA.
 AC AAU85120;
 DT 08-MAY-2002 (first entry)
 DT
 DE Human LAGE1 segment 3.
 KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
 KW viral infection; human immunodeficiency virus; melanoma;
 KW bacterial infection; Salmonella; Legionella; parasitic infection;

KM		Trypanosoma; Toxoplasma; Giardia.
XX		
OS	Homo sapiens.	
XX		
PN	WO200190197-A1.	
PD	29-NOV-2001.	
XX		
XX		
PF	25-MAY-2001; 2001WO-AU000622.	
XX		
PR	26-MAY-2000; 2000AU-00007761.	
PA	(AUSU) UNIV AUSTRALIAN NAT.	
PI	Thomson SA, Ramshaw IA;	
XX		
DR	WPI: 2002-147575/19.	
XX	N-PSDB, ABK36940.	
PT	New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a pathogen or cancer.	
PS	Example 3; Fig 27; 364pp; English.	
CC	The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked together in a different relationship relative to their linkage in the parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polynucleotide encoding and a computer system for designing the synthetic polypeptides. The synthetic polypeptides and polynucleotides are referred to as a Savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, oesophagus, brain, testicle, uterus), as potentiating agents.	
CC	Compositions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HIV (human immunodeficiency virus), hepatitis, influenza, Japanese encephalitis virus, Epstein-Barr virus and respiratory syncytial virus), bacterial (e.g., infections caused by Neisseria, Meningococcus, Haemophilus, Salmonella, Streptococcus, Legionella and Mycobacterium or parasitic (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,	
CC	Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is a peptide derived from a parent protein used to construct a savine of the invention	
CC		
CC		
SQ	Sequence 30 AA;	
XX		
Alignment Scores:		
Pred. No.:	6.1e-17	Length: 30
Score:	28.00	Matches: 28
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	15.56%	Indels: 0
DB:	5	Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x AAUB5120 (1-30)		
OY	GGCAATGCTGGCGGCCGACAGAGCGAGGTGCACACGGCGCAGAGAGTCCCCGGGCGCA	144
Dd		
	1 GtAAnaAlagIyGlPProoIyglunlaagIyAlatHnclYgIyArgcIyProntgIyAla	20
OY	145 GGGGCAAGCAGGGGCGCTGGGGCCG	168
Dd		
	21 GtYAlaAlaArGalAsercIyPro	28
RESULT 22		
AAUB5102		
ID	AAUB5102 standard; peptide; 30 AA	

XX	AAU85102;
AC	
XX	08-MAY-2002 (first entry)
DT	
XX	
DE	Human NYN501a segment 1.
XX	
KW	Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KM	viral infection; human immunodeficiency virus; melanoma;
KM	bacterial infection; Salmonella; Legionella; parasitic infection;
KM	Tyranosoma; Toxoplasma; Giardia.
XX	
OS	Homo sapiens.
XX	
PN	MO200190197-A1.
XX	
PD	29-NOV-2001.
XX	
PF	25-MAY-2001; 2001WO-AU000622.
XX	
PR	26-MAY-2000; 2000AU-00007761.
XX	
PA	(AUSU) UNIV AUSTRALIAN NAT.
XX	
PI	Thomson SA, Ramshaw IA;
XX	
DR	WPI; 2002-147575/19.
DR	N-PDSB; ABK36922.
XX	
PT	New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a pathogen or cancer.
FT	
PT	
XX	
PS	Example 3; Fig 27; 364pp; English.
XX	
CC	The invention relates to a new synthetic polypeptide (I) comprising several different segments of at least one parent polypeptide linked together in a different relationship relative to their linkage in the parent polypeptide to impede, abrogate or otherwise alter at least one function associated with the parent polypeptide and for inducing an immune response against a pathogen or cancer. Also included are a synthetic polynucleotide encoding and a computer system for designing the synthetic polypeptides. The synthetic polypeptides and polynucleotides are referred to as a Savine. The synthetic polypeptide is useful for modulating immune responses preferably directed against a pathogen or a cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head and neck, pancreas, prostate, stomach, bladder, kidney, bone liver, CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC	Compositions comprising the polypeptide may be used in the treatment or prophylaxis against viral (such as infections caused by HIV (human immunodeficiency virus), hepatitis, influenza, Japanese encephalitis virus, Epstein-Barr virus and respiratory syncytial virus), bacterial (e.g., infections caused by Neisseria, Meningococcal, Haemophilus, CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania, CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is a peptide derived from a parent protein used to construct a savine of the invention
CC	
XX	
SO	Sequence 30 AA;
Alignment Scores:	
Pred. No.:	6,1e-17 Length: 30
Score:	28.00 Matches: 28
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	15.56% Indels: 0
DB:	Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x AAU85102 (1-30)

1 ATGCGAGCCGAAGGCCGGGCGGCACAAGGGGGTTTCAGCGGGCAGATGCTGATGGCCCCAGAAGGC 60

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Db      3 MetGlnAlaGluGlyArgGlyThrGlySerThrGlyAspAlaAspGlyProGlyGly 22
QY      61 CCTGGATTCCTGATGGAGCCACAGG 84
      23 ProGlyIleProAspGlyProGly 30

RESULT 23
AAE07757
ID      AAE07757 standard; peptide; 27 AA.
XX
AC      AAE07757;
XX
DT      06-NOV-2001 (first entry)
XX
DE      Human HLA-DP restricted T cell epitope #2 of NY ESO-1 protein.
XX
KW      Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW      class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW      NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW      tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW      immunotherapy.
XX
OS      Homo sapiens.
XX
PN      WO200155393-A2.
XX
PD      02-AUG-2001.
XX
PF      26-JAN-2001; 2001WO-US002765.
XX
PR      28-JAN-2000; 2000US-0179004P.
XX      29-SEP-2000; 2000US-0237107P.
XX
PA      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI      Wang R, Rosenberg SA, Zeng G;
XX
DR      WPI; 2001-496851/54.
XX
PT      New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT      useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT      protection from metastasis.
XX
PS      Claim 91; Page 20; 134pp; English.
XX
CC      The invention relates to the identification and isolation of major
CC      histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC      epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC      from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC      antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC      restricted. The products of the gene are promising candidates for
CC      immunotherapeutic strategies for the prevention, treatment and diagnosis
CC      of patients with cancer. The cancer epitopes are useful as immunogen and
CC      vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC      lymphocytes resulting in protection of the recipient from development of
CC      cancer and protection from metastasis, or by inhibiting the growth of
CC      cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC      useful as diagnostic agent to detect the presence of cancer, to enhance
CC      the generation of antibody and/or CD8+ T cell responses against any given
CC      target antigen and/or hapten and to induce tumour-specific humoral-
CC      mediated immunity against cancer. The present sequence is human HLA-DP
CC      restricted T cell epitope of NY ESO-1 protein
XX
SQ      Sequence 27 AA;

Alignment Scores:
Pred. No.:      5,27e-16      Length:      27
Score:          27.00         Matches:      27
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    15.00%       Indels:      0
DB:             4            Gaps:        0

```

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US-10-023-182-1_COPY_54_593 (1-540) x AAE07757 (1-27)
QY      451 TCCTGTCTCCAGAGCCTTCCCTGTGATGATGATCAAGACAGTGCTTCTGCCGTGTT 510
      1 SerCysLeuGlnGlnIleuSerIleuMetIleThrGlnCysPheIleuProValPhe 20
Db      511 TTGGCTCAGCCTCCCTCAGAG 531
      21 LeuAlaGlnProProSerGly 27

RESULT 24
AAE07717
ID      AAE07717 standard; peptide; 27 AA.
XX
AC      AAE07717;
XX
DT      06-NOV-2001 (first entry)
XX
DE      Human NY ESO-1 MHC class II restricted T cell epitope #3.
XX
KW      Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW      class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW      NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW      tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW      immunotherapy.
XX
OS      Homo sapiens.
XX
PN      WO200155393-A2.
XX
PD      02-AUG-2001.
XX
PF      26-JAN-2001; 2001WO-US002765.
XX
PR      28-JAN-2000; 2000US-0179004P.
XX      29-SEP-2000; 2000US-0237107P.
XX
PA      (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI      Wang R, Rosenberg SA, Zeng G;
XX
DR      WPI; 2001-496851/54.
XX
PT      New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT      useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT      protection from metastasis.
XX
PS      Claim 4; Page 15; 134pp; English.
XX
CC      The invention relates to the identification and isolation of major
CC      histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC      epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC      from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC      antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC      restricted. The products of the gene are promising candidates for
CC      immunotherapeutic strategies for the prevention, treatment and diagnosis
CC      of patients with cancer. The cancer epitopes are useful as immunogen and
CC      vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC      lymphocytes resulting in protection of the recipient from development of
CC      cancer and protection from metastasis, or by inhibiting the growth of
CC      cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC      useful as diagnostic agent to detect the presence of cancer, to enhance
CC      the generation of antibody and/or CD8+ T cell responses against any given
CC      target antigen and/or hapten and to induce tumour-specific humoral-
CC      mediated immunity against cancer. The present sequence is MHC class II
CC      restricted T cell epitope of human NY ESO-1 protein
XX
SQ      Sequence 27 AA;

Alignment Scores:
Pred. No.:      5,27e-16      Length:      27
Score:          27.00         Matches:      27

```


Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.00% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x AAE07717 (1-27)

QY 331 CAGATGCCCCCGCTCCGTCAGAGGAGTTCAGTGTCCGAC 390
Db 1 GlnAplAProPleuProValProGlyValLeuLeuYsGluPheThrValSerGly 20

QY 391 AACATACGACTATCCGACTG 411
Db 21 AenileuThrIleArgLeu 27

RESULT 25

AAE07718
ID AAE07718 standard; peptide; 25 AA.
XX
XX AAE07718;
AC
XX 06-NOV-2001 (first entry)
DT
DE Human NY ESO-1 MHC class II restricted T cell epitope #4.
XX
XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
KM class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KM NY ESO-1 protein; CD4+ T lymphocyte; human leukocyte antigen; HLA;
KM tumour-specific humoral-mediated immunity; cancer; cytostatic;
XX immunotherapy.
XX
XX Homo sapiens.
OS
XX WO200155393-A2.
PN
XX 02-AUG-2001.
PD
XX 26-JAN-2001; 2001WO-US002765.
PF
XX 28-JAN-2000; 2000US-0179004P.
PR 29-SEP-2000; 2000US-0237107P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
PA
XX Wang R, Rosenberg SA, Zeng G;
PI WPI; 2001-496851/54.
DR
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT protection from metastasis.
XX
XX Claim 4; Page 16; 134pp; English.
XX
XX The invention relates to the identification and isolation of major
CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leukocyte
CC antigen (HLA) class II restricted manner. In particular HLA-DR or HLA-DP
CC restricted. The products of the gene are promising candidates for
CC immunotherapeutic strategies for the prevention, treatment and diagnosis
CC of patients with cancer. The cancer epitopes are useful as immunogen and
CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC lymphocytes resulting in protection of the recipient from development of
CC cancer and protection from metastasis, or by inhibiting the growth of
CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC useful as diagnostic agent to detect the presence of cancer, to enhance
CC the generation of antibody and/or CD8+ T cell responses against any given
CC target antigen and/or hapten and to induce tumour-specific humoral-
CC mediated immunity against cancer. The present sequence is MHC class II
CC restricted T cell epitope of human NY ESO-1 protein
XX
XX Sequence 25 AA;

Alignment Scores:
Pred. No.: 3.84e-14 Length: 25
Score: 25.00 Matches: 25
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 13.89% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x AAE07718 (1-25)

QY 337 GCCCCACCGCTCCCGTCAGAGGAGTTCGAGAGTTCAGTGTCCGACATA 396
Db 1 AlaProPleuProValProGlyValLeuLeuYsGluPheThrValSerGlyAsnIle 20

QY 397 CTGACTATCCGACTG 411
Db 21 LeuThrIleArgLeu 25

RESULT 26

ADD71521
ID ADD71521 standard; peptide; 25 AA.
XX
XX ADD71521;
AC
XX 15-JAN-2004 (first entry)
DT
DE HLA-DP4 binding peptide ligand #83.
XX
XX cytostatic; immunostimulant; immunosuppressive; neuroprotective;
KM antidiabetic; antiallergic; ligand; HLA-DP4; human leukocyte antigen;
KM immunomodulator; vaccine; pathogen; tumor cell; multiple sclerosis;
KM diabetes; allergy; graft rejection.
XX
XX Synthetic.
OS
XX FR2830940-A1.
PN
XX 18-APR-2003.
PD
XX 17-OCT-2001; 2001FR-00013352.
PF
XX 17-OCT-2001; 2001FR-00013352.
PR
XX 17-OCT-2001; 2001FR-00013352.
XX
XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
PA (SEDA-) SEDAC THERAPEUTICS SOC ETUD DEV ANTIGENE.
XX
XX Malliere B, Castelli F, Buhot C, Georges B;
PI WPI; 2003-395920/38.
DR
XX WPI; 2003-395920/38.
XX
XX Process for selecting ligands for human leukocyte antigen DP4, useful as
PT immunomodulators for treating e.g. tumors, based on inhibition of
PT binding.
XX
XX Disclosure; SEQ ID NO 83; 70pp; French.
XX
XX The invention relates to a process for selecting ligands (A) of HLA
CC (human leukocyte antigen)-DP4 comprising: (a) incubating purified DP4
CC with a labelled peptide (I) in presence of different concentrations of
CC test compounds; (b) separating complexes formed; (c) determining DP4-(I)
CC complexes by measuring a signal from the label; and (d) selecting
CC compounds having binding IC50 less than 1000 nM, corresponding to the
CC concentration required to inhibit 50 % binding of (I). (I) has signal-to-
CC noise ratio over 5, at 10 nM, in a direct binding test to DP4. (A) cause
CC activation of T cells, or their energy. (A), or nucleic acid that encodes
CC them, are useful as immunomodulators, including uses in vaccines against
CC pathogens and tumor cells, also for treating autoimmune diseases
CC (multiple sclerosis and type I diabetes), allergy and graft rejection.
CC (A) are useful as reagents for diagnosing the immune status of an
CC individual, while labelled complexes of DP4 with (A) are used to select
CC antigen-specific CD4+ T cells. The method identifies ligands specific for
CC HLA-DP4 and allows exact definition of the binding motif shared by DP4

patnogens and tumor cells, also for treating autoimmune diseases

compounds having binding IC_{50} less than 1000 nM, corresponding to the

CC concentration required to inhibit 50 % binding of (I). (I) has signal-to-noise ratio over 5, at 10 nM, in a direct binding test to DP4. (A) causes activation of T cells, or their anergy. (A), or nucleic acid that encodes them, are useful as immunomodulators, including uses in vaccines against pathogens and tumor cells, also for treating autoimmune diseases (multiple sclerosis and type I diabetes), allergy and graft rejection. (A) are useful as reagents for diagnosing the immune status of an individual, while labelled complexes of DP4 with (A) are used to select antigen-specific CD4+ T cells. The method identifies ligands specific for HLA-DP4 and allows exact definition of the binding motif shared by DP4 binding ligands. This sequence represents an example of a peptide ligand of the invention. The peptides are labelled (biotinylated) at their N-termini.

SQ Sequence 25 AA;

Alignment Scores:

Pred. No.:	3.84e-14	Length:	25
Score:	25.00	Matches:	25
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	13.89%	Indels:	0
DB:	7	Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) x ADD71532 (1-25)

OY 259 CTGCTTGAGTTCTACCTCGCATGCGCTTTCGGCAGACCCAGAGAGCTGCGCCG 318
|||
Db 1 LeuLeuGluPheTyrLeuAlaMetProPheAlaTrpMetGluAlaGluLeuAlaArg 20
|||

OY 319 AGGAGCTTGCGCCGAG 333
|||
Db 21 ArgSerLeuAlaGln 25
|||

RESULT 29

AAU85128
ID AAU85128 standard; peptide; 30 AA.
AC AAU85128;
XX
XX 08-MAY-2002 (first entry)
DT
XX Human LAGE1 segment 11.
DE
XX
XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficiency virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
XX
XX Homo sapiens.
OS
XX
XX WO200190197-A1.
PN
XX
XX 29-NOV-2001.
PD
XX
XX 25-MAY-2001; 2001WO-AU000622.
PF
XX 26-MAY-2000; 2000AU-00007761.
PR
XX (AUSU) UNIV AUSTRALIAN NAT.
PA
XX Thomson SA, Ramshaw IA,
XX
XX
XX MPI, 2002-147575/19.
DR
XX N-P8DB; ABK36948.
DR
XX
XX
XX New synthetic polypeptides having several different segments of at least one parent polypeptide linked together differently compared to the linkage in the parent polypeptide, for inducing immune response against a pathogen or cancer.
PT
XX
XX Example 3; Fig 27; 364pp; English.
PS
XX

CC The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium) or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention

SQ Sequence 30 AA;

Alignment Scores:

Pred. No.:	3.73e-14	Length:	30
Score:	25.00	Matches:	25
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	13.89%	Indels:	0
DB:	5	Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) x AAU85128 (1-30)

OY 445 ATCAGCTCTGTCTTCAGCAGAGCTTCCCTGTGATGATCAGCAGTCTTTCGCC 504
|||
Db 1 IleSerSerCysLeuGlnGlnLeuSerLeuMetTrpIleTrpGlnCysPheLeuPro 20
|||

OY 505 GTGTTTTCGCTCAG 519
|||
Db 21 ValPheLeuAlaGln 25
|||

RESULT 30

ADD71520
ID ADD71520 standard; peptide; 23 AA.
AC ADD71520;
XX
XX
XX 15-JAN-2004 (first entry)
DT
XX
XX
XX HLA-DP4 binding peptide ligand #82.
DE
XX
XX cytosolic; immunostimulant; immunosuppressive; neuroprotective;
KW antidiabetic; anti-allergic; ligand; HLA-DP4; human leukocyte antigen;
KW immunomodulator; vaccine; pathogen; tumor cell; multiple sclerosis;
KW diabetes; allergy; graft rejection.
XX
XX Synthetic.
OS
XX
XX FR2830940-A1.
PN
XX
XX 18-APR-2003.
PD
XX
XX 17-OCT-2001; 2001FR-00013352.
PF
XX
XX 17-OCT-2001; 2001FR-00013352.
PR
XX (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
PA (SEDA-) SEDAC THERAPEUTICS SOC ETUD DEV ANTIGENE.
XX
XX Maille B, Castelli F, Bubot C, Georges B;
PI

```
XX DR WPI; 2003-395920/38.
XX
XX PT Process for selecting ligands for human leukocyte antigen DP4, useful as
XX PT immunomodulators for treating e.g. tumors, based on inhibition of
XX PT binding.
XX PS Disclosure; SEQ ID NO 82; 70pp; French.
XX
XX CC The invention relates to a process for selecting ligands (A) of HLA
XX CC (human leukocyte antigen)-DP4 comprising: (a) incubating purified DP4
XX CC with a labelled peptide (I) in presence of different concentrations of
XX CC test compounds; (b) separating complexes formed; (c) determining DP4-(I)
XX CC complexes by measuring a signal from the label; and (d) selecting
XX CC compounds having binding IC50 less than 1000 nM, corresponding to the
XX CC concentration required to inhibit 50 % binding of (I). (I) has signal-to-
XX CC noise ratio over 5, at 10 nM, in a direct binding test to DP4. (A) causes
XX CC activation of T cells, or their anergy. (A), or nucleic acid that encodes
XX CC them, are useful as immunomodulators, including uses in vaccines against
XX CC pathogens and tumor cells, also for treating autoimmune diseases
XX CC (multiple sclerosis and type I diabetes), allergy and graft rejection.
XX CC (A) are useful as reagents for diagnosing the immune status of an
XX CC individual, while labelled complexes of DP4 with (A) are used to select
XX CC antigen-specific CD4+ T cells. The method identifies ligands specific for
XX CC HLA-DP4 and allows exact definition of the binding motif shared by DP4
XX CC binding ligands. This sequence represents an example of a peptide ligand
XX CC of the invention. The peptides are labelled (biotinylated) at their N-
XX CC terminl.
XX
XX SQ Sequence 23 AA;
XX
XX Alignment Scores:
XX Pred. No.: 2,81e-12 Length: 23
XX Score: 23.00 Matches: 23
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 12.78% Indels: 0
XX DB: 7 Gaps: 0
XX
XX US-10-023-182-1_COPY_54_593 (1-540) x ADD71520 (1-23)
XX
XX QY 472 CHTGTGATGTGATCAGCGAGTTCCTTTCGCCGCTTTTGGCTCAGGCTCCCTCAGGG 531
XX DB 1 LeuLeuMetTrpIleThrGlnCysPheLeuProValPheLeuAlaGlnProProSergly 20
XX
XX QY 532 CAGAGCGCG 540
XX DB 21 GlnArgArg 23
XX
XX RESULT 31
XX AAU85118
XX ID AAU85118 standard; peptide; 30 AA.
XX AC AAU85118;
XX
XX DT 08-MAY-2002 (first entry)
XX
XX DE Human LAGE1 segment 1.
XX
XX KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
XX KW viral infection; human immunodeficiency virus; melanoma;
XX KW bacterial infection; Salmonella; Legionella; parasitic infection;
XX KW Trypanosoma; Toxoplasma; Giardia.
XX
XX OS Homo sapiens.
XX
XX PN WO200190197-A1.
XX
XX PD 29-NOV-2001.
XX
XX PF 25-MAY-2001; 2001WO-AU000622.
XX
XX PR 26-MAY-2000; 2000AU-00007761.
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XX
XX PA (AUSU ) UNIV AUSTRALIAN NAT.
XX
XX PI Thomson SA, Ramshaw IA;
XX
XX DR WPI; 2002-147575/19.
XX DR N-PSDB; ABK36938.
XX
XX PT New synthetic polypeptides having several different segments of at least
XX PT one parent polypeptide linked together differently compared to the
XX PT linkage in the parent polypeptide, for inducing immune response against a
XX PT pathogen or cancer.
XX
XX PS Example 3; Fig 27; 364pp; English.
XX
XX CC The invention relates to a new synthetic polypeptide (I) comprising
XX CC several different segments of at least one parent polypeptide linked
XX CC together in a different relationship relative to their linkage in the
XX CC parent polypeptide to impede, abrogate or otherwise alter at least one
XX CC function associated with the parent polypeptide and for inducing an
XX CC immune response against a pathogen or cancer. Also included are a
XX CC synthetic polynucleotide encoding and a computer system for designing the
XX CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
XX CC are referred to as a Savine. The synthetic polypeptide is useful for
XX CC modulating immune responses preferably directed against a pathogen or a
XX CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
XX CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
XX CC oesophagus, brain, testicle, uterus), as potentiating agents.
XX CC Compositions comprising the polypeptide may be used in the treatment or
XX CC prophylaxis against viral (such as infections caused by HIV (human
XX CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
XX CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
XX CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
XX CC Salmonella, Streptococcal, Legionella and Mycobacterium) or parasitic
XX CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
XX CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
XX CC a peptide derived from a parent protein used to construct a savine of the
XX CC invention
XX
XX SQ Sequence 30 AA;
XX
XX Alignment Scores:
XX Pred. No.: 2,28e-11 Length: 30
XX Score: 22.00 Matches: 22
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 12.22% Indels: 0
XX DB: 5 Gaps: 0
XX
XX US-10-023-182-1_COPY_54_593 (1-540) x AAU85118 (1-30)
XX
XX QY 19 GGCACAGGGGGTTGAGCGCGGATGATGCGCCAGAGGCGCTGGCATTCGTGATGC 78
XX DB 9 GlyThrGlyGlySerThrGlnGlyAspAlaSpolYProGlyGlyProGlyIleProAspIly 28
XX
XX QY 79 CCAGCG 84
XX DB 29 ProGly 30
XX
XX RESULT 32
XX ADD71449
XX ID ADD71449 standard; peptide; 21 AA.
XX AC ADD71449;
XX
XX DT 15-JAN-2004 (first entry)
XX
XX DE HLA-DP4 binding peptide ligand #11.
XX
XX KW cycostatic; immunostimulant; immunosuppressive; neuroprotective;
XX KW antidiabetic; antiallergic; ligand; HLA-DP4; human leukocyte antigen;
XX KW immunomodulator; vaccine; pathogen; tumor cell; multiple sclerosis;
XX KW diabetes; allergy; graft rejection.
```



```
XX DE Human ESO p156-175 peptide, to identify MHC class II-restricted epitopes.
XX XX
XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
XX class II restricted T cell epitope; MHC-II epitope; cancer antigen;
XX NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
XX tumour-specific humoral-mediated immunity; cancer; cytostatic;
XX immunotherapy.
XX Homo sapiens.
XX WO200155393-A2.
XX PD 02-AUG-2001.
XX PF 26-JAN-2001; 2001WO-US002765.
XX PR 28-JAN-2000; 2000US-0179004P.
XX PR 29-SEP-2000; 2000US-0237107P.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA Wang R, Rosenberg SA, Zeng G;
XX PI WPI; 2001-496851/54.
XX DR
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
XX PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
XX PT protection from metastasis.
XX
XX Example 3; Fig 3; 134pp; English.
XX
XX The invention relates to the identification and isolation of major
XX histocompatibility (MHC) class II restricted T cell epitope (MHC-II
XX epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
XX from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
XX antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
XX restricted. The products of the gene are promising candidates for
XX immunotherapeutic strategies for the prevention, treatment and diagnosis
XX of patients with cancer. The cancer epitopes are useful as immunogen and
XX vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
XX lymphocytes resulting in protection of the recipient from development of
XX cancer and protection from metastasis, or by inhibiting the growth of
XX cells expressing the NY-ESO-1 gene product. The cancer peptides are also
XX useful as diagnostic agent to detect the presence of cancer, to enhance
XX the generation of antibody and/or CD8+ T cell responses against any given
XX target antigen and/or hapten and to induce tumour-specific humoral-
XX mediated immunity against cancer. The present sequence is human ESO p156-
XX 175 peptide used in the identification of putative MHC class II -
XX restricted epitopes from HLA-DR4-transgenic mice
XX
XX SQ Sequence 20 AA;
XX
XX Alignment Scores:
XX Pred. No.: 1.76e-09 Length: 20
XX Score: 20.00 Matches: 20
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 11.11% Indels: 0
XX DB: 4 Gaps: 0
XX
XX US-10-023-182-1_COPY_54_593 (1-540) x AAE07744 (1-20)
XX
XX QY 466 CTTTCCCTGATGATGATACGACGATGCTTCTCCGCTTTTGGCTCAGCCTCC 525
XX Db 1 leuSeIleuLeuMetTrpIleThrGlnCysPheLeuProValPheLeuAlaGlnProPro 20
XX
XX RESULT 35
XX AAE07746 standard; peptide; 20 AA.
XX ID AAE07746;
XX AC AAE07746;
XX XX
```

```
DT 06-NOV-2001 (first entry)
XX XX
XX Human ESO p111-130 peptide to generate CD4+T cells specific for NY ESO-1.
XX XX
XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
XX class II restricted T cell epitope; MHC-II epitope; cancer antigen;
XX NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
XX tumour-specific humoral-mediated immunity; cancer; cytostatic;
XX immunotherapy.
XX Homo sapiens.
XX WO200155393-A2.
XX PN
XX PD 02-AUG-2001.
XX PF 26-JAN-2001; 2001WO-US002765.
XX PR 28-JAN-2000; 2000US-0179004P.
XX PR 29-SEP-2000; 2000US-0237107P.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PA Wang R, Rosenberg SA, Zeng G;
XX PI WPI; 2001-496851/54.
XX DR
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
XX PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
XX PT protection from metastasis.
XX
XX Example 4; Fig 4B; 134pp; English.
XX
XX The invention relates to the identification and isolation of major
XX histocompatibility (MHC) class II restricted T cell epitope (MHC-II
XX epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
XX from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
XX antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
XX restricted. The products of the gene are promising candidates for
XX immunotherapeutic strategies for the prevention, treatment and diagnosis
XX of patients with cancer. The cancer epitopes are useful as immunogen and
XX vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
XX lymphocytes resulting in protection of the recipient from development of
XX cancer and protection from metastasis, or by inhibiting the growth of
XX cells expressing the NY-ESO-1 gene product. The cancer peptides are also
XX useful as diagnostic agent to detect the presence of cancer, to enhance
XX the generation of antibody and/or CD8+ T cell responses against any given
XX target antigen and/or hapten and to induce tumour-specific humoral-
XX mediated immunity against cancer. The present sequence is human ESO p111-
XX 130 peptide used in the generation of human CD4+T cells specific for NY
XX ESO-1 protein
XX
XX SQ Sequence 20 AA;
XX
XX Alignment Scores:
XX Pred. No.: 1.76e-09 Length: 20
XX Score: 20.00 Matches: 20
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 11.11% Indels: 0
XX DB: 4 Gaps: 0
XX
XX US-10-023-182-1_COPY_54_593 (1-540) x AAE07746 (1-20)
XX
XX QY 331 CAGATGCGCCACCGCTCCGCTGCGAGGAGTCTCGAAGAGTTCACTGTGCGCGC 390
XX Db 1 GlnAspAlaProLeuProValProGlyValLeuLeuLysGlnPheThrValSerGly 20
XX
XX RESULT 36
XX AAE07743 standard; peptide; 20 AA.
XX ID AAE07743;
XX AC AAE07743;
XX XX
```

```
XX 06-NOV-2001 (first entry)
XX Human ESO p131-150 peptide, to identify MHC class II-restricted epitopes.
DE
XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
XX class II restricted T cell epitope; MHC-II epitope; cancer antigen;
XX NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
XX tumour-specific humoral-mediated immunity; cancer; cytostatic;
XX immunotherapy.
XX Homo sapiens.
XX MO200155393-A2.
XX 02-AUG-2001.
XX 26-JAN-2001; 2001WO-US002765.
XX 28-JAN-2000; 2000US-0179004P.
XX 29-SEP-2000; 2000US-0237107P.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Wang R, Rosenberg SA, Zeng G;
XX WPI; 2001-496851/54.
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
XX useful as immunogen and vaccine for inhibiting cancer in a mammal or as
XX protection from metastasis.
XX Example 3; Fig 3; 134pp; English.
XX
XX The invention relates to the identification and isolation of major
XX histocompatibility (MHC) class II restricted T cell epitope (MHC-II
XX epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
XX from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
XX antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
XX restricted. The products of the gene are promising candidates for
XX immunotherapeutic strategies for the prevention, treatment and diagnosis
XX of patients with cancer. The cancer epitopes are useful as immunogen and
XX vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
XX lymphocytes resulting in protection of the recipient from development of
XX cancer and protection from metastasis, or by inhibiting the growth of
XX cells expressing the NY-ESO-1 gene product. The cancer peptides are also
XX useful as diagnostic agent to detect the presence of cancer, to enhance
XX the generation of antibody and/or CD8+ T cell responses against any given
XX target antigen and/or happen and to induce tumour-specific humoral-
XX mediated immunity against cancer. The present sequence is human ESO p131-
XX 150 peptide used in the identification of putative MHC class II -
XX restricted epitopes from HLA-DR4-transgenic mice
XX
XX Sequence 20 AA;
SQ
XX
XX Alignment Scores:
XX Pred. No.: 1.76e-09 Length: 20
XX Score: 20.00 Matches: 20
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 11.11% Indels: 0
XX DB: 4 Gaps: 0
XX
XX US-10-023-182-1_COPY_54_593 (1-540) x AAE07731 (1-20)
XX
XX 391 AACATAGTGCATGCGACTGCTGCAGACCAAGCCGCACTGCTCCATCAGC 450
XX |||||
XX 1 AsnIleuThrIleArgLeuThrAlaAlaAspHisArgGlnLeuGlnLeuSerIleSer 20
XX
XX RESULT 37
XX AAE07731
XX ID AAE07731 standard; peptide; 20 AA.
XX
```

```
AC AAE07731;
XX 06-NOV-2001 (first entry)
XX Human NY ESO-1 MHC class II restricted T cell epitope #17.
DE
XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
XX class II restricted T cell epitope; MHC-II epitope; cancer antigen;
XX NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
XX tumour-specific humoral-mediated immunity; cancer; cytostatic;
XX immunotherapy.
XX Homo sapiens.
XX MO200155393-A2.
XX 02-AUG-2001.
XX 26-JAN-2001; 2001WO-US002765.
XX 28-JAN-2000; 2000US-0179004P.
XX 29-SEP-2000; 2000US-0237107P.
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX Wang R, Rosenberg SA, Zeng G;
XX WPI; 2001-496851/54.
XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
XX useful as immunogen and vaccine for inhibiting cancer in a mammal or as
XX protection from metastasis.
XX Claim 4; Fig 3; 134pp; English.
XX
XX The invention relates to the identification and isolation of major
XX histocompatibility (MHC) class II restricted T cell epitope (MHC-II
XX epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
XX from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
XX antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
XX restricted. The products of the gene are promising candidates for
XX immunotherapeutic strategies for the prevention, treatment and diagnosis
XX of patients with cancer. The cancer epitopes are useful as immunogen and
XX vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
XX lymphocytes resulting in protection of the recipient from development of
XX cancer and protection from metastasis, or by inhibiting the growth of
XX cells expressing the NY-ESO-1 gene product. The cancer peptides are also
XX useful as diagnostic agent to detect the presence of cancer, to enhance
XX the generation of antibody and/or CD8+ T cell responses against any given
XX target antigen and/or happen and to induce tumour-specific humoral-
XX mediated immunity against cancer. The present sequence is MHC class II
XX restricted T cell epitope (ESO p141-160) of human NY ESO-1 protein
XX
XX Sequence 20 AA;
SQ
XX
XX Alignment Scores:
XX Pred. No.: 1.76e-09 Length: 20
XX Score: 20.00 Matches: 20
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 11.11% Indels: 0
XX DB: 4 Gaps: 0
XX
XX US-10-023-182-1_COPY_54_593 (1-540) x AAE07731 (1-20)
XX
XX 421 GACCAAGCGCAATGCGAGCTGCTGCATGCTGCTCCAGCAGCTTTCCTGTGATG 480
XX |||||
XX 1 AspHisArgGlnLeuGlnLeuSerIleSerSerGlySerGlnGlnLeuSerLeuMet 20
XX
XX RESULT 38
XX AAE07729
XX ID AAE07729 standard; peptide; 20 AA.
XX
```

```
AC AAE07729;
XX
XX 06-NOV-2001 (first entry)
XX
DE Human NY ESO-1 MHC class II restricted T cell epitope #15.
XX
XX Human, major histocompatibility complex; MHC; vaccine; metastasis;
XX class II restricted T cell epitope; MHC-II epitope; cancer antigen;
XX NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
XX tumour-specific humoral-mediated immunity; cancer; cytostatic;
XX immunotherapy.
XX
OS Homo sapiens.
XX
XX WO200155393-A2.
XX
XX 02-AUG-2001.
XX
XX 26-JAN-2001; 2001WO-US002765.
XX
XX 28-JAN-2000; 2000US-0179004P.
XX 29-SEP-2000; 2000US-0237107P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wang R, Rosenberg SA, Zeng G;
XX
XX WPI; 2001-496851/54.
XX
XX
XX Claim 4; Fig 3; 134p; English.
XX
XX The invention relates to the identification and isolation of major
XX histocompatibility (MHC) class II restricted T cell epitope (MHC-II
XX epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
XX from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
XX antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
XX restricted. The products of the gene are promising candidates for
XX immunotherapeutic strategies for the prevention, treatment and diagnosis
XX of patients with cancer. The cancer epitopes are useful as immunogen and
XX vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
XX lymphocytes resulting in protection of the recipient from development of
XX cancer and protection from metastasis, or by inhibiting the growth of
XX cells expressing the NY-ESO-1 gene product. The cancer peptides are also
XX useful as diagnostic agent to detect the presence of cancer, to enhance
XX the generation of antibody and/or CD8+ T cell responses against any given
XX target antigen and/or hapten and to induce tumour-specific humoral-
XX mediated immunity against cancer. The present sequence is MHC class II
XX restricted T cell epitope (ESO p116-135) of human NY ESO-1 protein
XX
SQ Sequence 20 AA;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1.76e-09 Length: 20
XX Score: 20.00 Matches: 20
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 11.11% Indels: 0
XX DB: 4 Gaps: 0
XX
XX US-10-023-182-1_COPY_54_593 (1-540) x AAE07729 (1-20)
XX
QY 346 CTTCCCGTCGCGGGGTGTTCTGAAGAGTCACTGCTCGGGAACATGACTGATC 405
XX |||||||
XX Db 1 LeupovalProGlyValLeuLeuYsgInPheThrValSerGlyAsnIleuThrIle 20
XX |||||||
XX
XX RESULT 39
XX AAE07742
XX ID AAE07742 standard; peptide; 20 AA.
XX
```

```
AC AAE07742;
XX
XX 06-NOV-2001 (first entry)
XX
XX
DE Human ESO p126-145 peptide, to identify MHC class II-restricted epitopes.
XX
XX Human, major histocompatibility complex; MHC; vaccine; metastasis;
XX class II restricted T cell epitope; MHC-II epitope; cancer antigen;
XX NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
XX tumour-specific humoral-mediated immunity; cancer; cytostatic;
XX immunotherapy.
XX
XX Homo sapiens.
XX
XX WO200155393-A2.
XX
XX 02-AUG-2001.
XX
XX 26-JAN-2001; 2001WO-US002765.
XX
XX 28-JAN-2000; 2000US-0179004P.
XX 29-SEP-2000; 2000US-0237107P.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Wang R, Rosenberg SA, Zeng G;
XX
XX WPI; 2001-496851/54.
XX
XX
XX Example 3; Fig 3; 134p; English.
XX
XX The invention relates to the identification and isolation of major
XX histocompatibility (MHC) class II restricted T cell epitope (MHC-II
XX epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
XX from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
XX antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
XX restricted. The products of the gene are promising candidates for
XX immunotherapeutic strategies for the prevention, treatment and diagnosis
XX of patients with cancer. The cancer epitopes are useful as immunogen and
XX vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
XX lymphocytes resulting in protection of the recipient from development of
XX cancer and protection from metastasis, or by inhibiting the growth of
XX cells expressing the NY-ESO-1 gene product. The cancer peptides are also
XX useful as diagnostic agent to detect the presence of cancer, to enhance
XX the generation of antibody and/or CD8+ T cell responses against any given
XX target antigen and/or hapten and to induce tumour-specific humoral-
XX mediated immunity against cancer. The present sequence is human ESO
XX 145 peptide used in the identification of putative MHC class II -
XX restricted epitopes from HLA-DR4-transgenic mice
XX
SQ Sequence 20 AA;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1.76e-09 Length: 20
XX Score: 20.00 Matches: 20
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 11.11% Indels: 0
XX DB: 4 Gaps: 0
XX
XX US-10-023-182-1_COPY_54_593 (1-540) x AAE07742 (1-20)
XX
QY 376 TTCACTGTGTCGCGGACATATGACTGATCGGACTGACTGCGACACCGCAACTG 435
XX |||||||
XX Db 1 PheThrValSerGlyAsnIleuThrIleArgLeuThrIleAlaAspHisArgGlnIleu 20
XX |||||||
XX
XX RESULT 40
XX AAE07747
XX ID AAE07747 standard; peptide; 20 AA.
XX
```


AC AAE07747;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human ESO p91-110 peptide to generate CD4+T cells specific for NY ESO-1.
 XX
 KW Human; major histocompatibility complex; MHC; vaccine; metastasis;
 KW class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 KW NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 KW tumour-specific humoral-mediated immunity; cancer; cytostatic;
 KW immunotherapy.
 XX
 OS Homo sapiens.
 XX
 PN WO200155393-A2.
 XX
 PD 02-AUG-2001.
 XX
 PF 26-JAN-2001; 2001WO-US002765.
 XX
 PR 28-JAN-2000; 2000US-017904P.
 XX
 PR 29-SEP-2000; 2000US-0237107P.
 XX
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 PI Wang R, Rosenberg SA, Zeng G;
 XX
 DR WPI; 2001-496851/54.
 XX
 PT New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 XX
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 XX
 PT protection from metastasis.
 XX
 PS Example 4; Fig 4B; 134pp; English.
 XX
 CC The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD8+ T cell responses against any given
 CC target antigen and/or hapten and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is human ESO p91-
 CC 110 peptide used in the generation of human CD4+T cells specific for NY
 CC ESO-1 protein
 CC
 XX
 SQ Sequence 20 AA;
 XX
 Alignment Scores:
 Pred. No.: 1,76e-09 Length: 20
 Score: 20,00 Matches: 20
 Percent Similarity: 100,00% Conservative: 0
 Best Local Similarity: 100,00% Mismatches: 0
 Query Match: 11,11% Indels: 0
 DB: 4 Gaps: 0
 US-10-023-182-1_COPY_54_593 (1-540) x AAE07747 (1-20)
 QY 271 TACCTGCCAATGCTTTGCGAGACCCATGAGAAGAGAGCTGCGCCGAGAGCGCTGAGC 330
 Db 1 TytleuhalmetetrohealathrProwetGtluhalglutueuhalatargtSerueuila 20
 RESULT_41
 AAE07741

```

ID  AAE07741 standard; peptide; 20 AA.
XX
XX  AAE07741;
AC
XX
XX  06-NOV-2001 (first entry)
DT
XX
XX  Human ESO p82-101 peptide, to identify MHC class II-restricted epitopes.
DE
XX
XX  Human; major histocompatibility complex; MHC; vaccine; metastasis;
KW  class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW  NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW  tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW  immunotherapy.
KM
XX
XX  Homo sapiens.
OS
XX
XX  WO200155393-A2.
PN
XX
XX  02-AUG-2001.
PD
XX
XX  26-JAN-2001; 2001WO-US002765.
PF
XX
XX  28-JAN-2000; 2000US-017900AP.
PR
XX  29-SEP-2000; 2000US-0237107F.
PR
XX
XX  (US$H ) US DEPT HEALTH & HUMAN SERVICES.
PA
XX
XX  Wang R, Rosenberg SA, Zeng G;
PI
XX  WPI; 2001-496851/54.
DR
XX
XX  New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT  useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT  protection from metastasis.
XX
XX
XX  Example 3; Fig 3; 134pp; English.
PS
XX
XX  The invention relates to the identification and isolation of major
CC  histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC  epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC  from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC  antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC  restricted. The products of the gene are promising candidates for
CC  immunotherapeutic strategies for the prevention, treatment and diagnosis
CC  of patients with cancer. The cancer epitopes are useful as immunogen and
CC  vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC  lymphocytes resulting in protection of the recipient from development of
CC  cancer and protection from metastasis, or by inhibiting the growth of
CC  cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC  useful as diagnostic agent to detect the presence of cancer, to enhance
CC  the generation of antibody and/or CD8+ T cell responses against any given
CC  target antigen and/or happen and to induce tumour-specific humoral-
CC  mediated immunity against cancer. The present sequence is human ESO p82-
CC  101 peptide used in the identification of putative MHC class II -
CC  restricted epitopes from HLA-DR4-transgenic mice
XX
XX
SQ  Sequence 20 AA;

Alignment Scores:
Pred. No.:      1.76e-09      Length:      20
Score:          20.00         Matches:      20
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00% Mismatches:      0
Query Match:     11.11%      Indels:       0
DB:              4           Gaps:        0

US-10-023-182-1_COPY_54_593 (1-540) x AAE07741 (1-20)

Oy      241 AGAGGGGCGGAGAGCGCGCTGTTAGATTCTACCTCGCGCATGCTTGGGAGACACGATG 300
Db      1  ArgGlyProGluSerArgIgneuInduInhefryrLeuAlaMetProPheAlaTrnPromet 20

RESULT 42

```

ID	AAE07732
XX	AAE07732 standard; peptide; 20 AA.
AC	
XX	AAE07732;
DT	
XX	06-NOV-2001 (first entry)
XX	
DE	Human NY ESO-1 MHC class II restricted T cell epitope #18.
KW	Human; major histocompatibility complex; MHC; vaccine; metastasis;
KM	Class II restricted T cell epitope; MHC-II epitope; cancer antigen;
KW	Ny ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
KW	tumour-specific humoral-mediated immunity; cancer; cytostatic;
KW	immunotherapy.
XX	
OS	Homo sapiens.
XX	
PN	WO200155393-A2.
XX	
PD	02-AUG-2001.
XX	
PF	26-JAN-2001; 2001MO-US002765.
XX	
PR	28-JAN-2000; 2000US-0179004P.
PR	29-SEP-2000; 2000US-0237107P.
XX	
PA	(USSH) US DEPT HEALTH & HUMAN SERVICES.
PI	
PT	Wang R, Rosenberg SA, Zeng G;
DR	WPI; 2001-496851/54.
XX	
XX	New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
PT	useful as immunogen and vaccine for inhibiting cancer in a mammal or as
PT	protection from metastasis.
PS	
XX	Claim 4; Fig 3; 13app; English.
CC	The invention relates to the identification and isolation of major
CC	histocompatibility (MHC) class II restricted T cell epitope (MHC-II
CC	epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
CC	from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
CC	antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
CC	restricted. The products of the gene are promising candidates for
CC	immunotherapeutic strategies for the prevention, treatment and diagnosis
CC	of patients with cancer. The cancer epitopes are useful as immunogen and
CC	vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
CC	lymphocytes resulting in protection of the recipient from development of
CC	cancer and protection from metastasis, or by inhibiting the growth of
CC	cells expressing the NY-ESO-1 gene product. The cancer peptides are also
CC	useful as diagnostic agent to detect the presence of cancer; to enhance
CC	the generation of antibody and/or CD8+ T cell responses against any given
CC	target antigen and/or hapten and to induce tumour-specific humoral-
CC	mediated immunity against cancer. The present sequence is MHC class II
CC	restricted T cell epitope (ESO 161-180) of human NY ESO-1 protein
XX	
SQ	Sequence 20 AA;
XX	
Alignment Scores:	
Pred. No.:	1,76e-09 Length: 20
Score:	20.00 Matches: 20
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	11.11% Indels: 0
DB:	4 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x AAE07732 (1-20)	
CY	481 TGAGTACGAGAGGCTTCGGCGCGGTGTTGGTGTCACGCTCCTCAAGGCGAGAAGGCGC 540
DJ	
Db	1 TrrpleThrIncyspheLeuProValPheIeuAlaIGlnProProSerGlyGIInArgXg 20
RESULT	43

AAE07745 ID AAE07745 standard; peptide; 20 AA.
 AC
 XX AAE07745;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human ESO p146-165 peptide, to identify MHC class II-restricted epitopes.
 XX
 XX Human; major histocompatibility complex; MHC; vaccine; metastasis;
 XX Class II restricted T cell epitope; MHC-II epitope; cancer antigen;
 XX NY ESO-1 protein; CD4+ T lymphocyte; human leucocyte antigen; HLA;
 XX tumour-specific humoral-mediated immunity; cancer; cytostatic;
 XX immunotherapy.
 XX
 XX Homo sapiens.
 OS
 XX MO200155393-A2.
 PN
 XX 02-AUG-2001.
 PD
 XX 26-JAN-2001; 2001WO-US002765.
 PF
 XX 28-JAN-2000; 2000US-0179004P.
 PR
 XX 29-SEP-2000; 2000US-0237107P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 PA
 XX Wang R, Rosenberg SA, Zeng G;
 P1
 XX WPI; 2001-496851/54.
 DR
 XX New NY-ESO cancer peptide or MHC class II restricted T cell epitopes,
 PT useful as immunogen and vaccine for inhibiting cancer in a mammal or as
 PT protection from metastasis.
 XX
 XX Example 3; Fig 3; 134dp; English.
 XX
 CC The invention relates to the identification and isolation of major
 CC histocompatibility (MHC) class II restricted T cell epitope (MHC-II
 CC epitope) derived from the cancer antigen, NY ESO-1. The MHC-II epitopes
 CC from NY ESO-1 are recognised by CD4+ T lymphocytes in an human leucocyte
 CC antigen (HLA) class II restricted manner, in particular HLA-DR or HLA-DP
 CC restricted. The products of the gene are promising candidates for
 CC immunotherapeutic strategies for the prevention, treatment and diagnosis
 CC of patients with cancer. The cancer epitopes are useful as immunogen and
 CC vaccine to inhibit or to prevent cancer in a mammal by eliciting CD4+ T
 CC lymphocytes resulting in protection of the recipient from development of
 CC cancer and protection from metastasis, or by inhibiting the growth of
 CC cells expressing the NY-ESO-1 gene product. The cancer peptides are also
 CC useful as diagnostic agent to detect the presence of cancer, to enhance
 CC the generation of antibody and/or CD4+ T cell responses against any given
 CC target antigen and/or hapten and to induce tumour-specific humoral-
 CC mediated immunity against cancer. The present sequence is human ESO p146-
 CC 165 peptide used in the identification of putative MHC class II -
 CC restricted epitopes from HLA-DR4-transgenic mice
 XX
 XX Sequence 20 AA;
 SQ
 Alignment Scores:
 Pred. No.: 1.76e-09 Length: 20
 Score: 20.00 Matches: 20
 Percent Similarity: 100.00% Conservative: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 11.11% Indels: 0
 DB: 4 Gaps: 0
 US-10-023-182-1_COPY_54_593 (1-540) x AAE07745 (1-20)
 436 CAGCTCTCATACAGCTCCGCTGTCAGAGAGCTTCCGCTGATGTGATCAGCAGTGC 495
 1 GlnIleuSerIleuSerCysIeuGlnGlnIleuSerIleuLeuMetTrpPleuThrGlnCys 20

RESULT 44
ADD71448
ID ADD71448 standard; peptide, 20 AA.
XX
AC
XX ADD71448;
XX
DN 15-JAN-2004 (first entry)
XX
DE HLA-DP4 binding peptide ligand #10.
XX
KW cytostatic; immunostimulant; immunosuppressive; neuroprotective;
KV antidiabetic; anti-allergic; ligand; HLA-DP4; human leukocyte antigen;
KW immunomodulator; vaccine; pathogen; tumor cell; multiple sclerosis;
KM diabetes; allergy; graft rejection.
XX
OS Synthetic.
XX
PN FR2830940-A1.
XX
PD 18-APR-2003.
XX
PE 17-OCT-2001; 2001FR-00013352.
XX
PR 17-OCT-2001; 2001FR-00013352.
XX
PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.
XX (SEDA-) SEDAC THERAPEUTICS SOC ETUD DEV ANTIGENE.
PI Maille B, Castella F, Buhot C, Georges B;
XX WPI: 2003-395920/38.
DR
XX Process for selecting ligands for human leukocyte antigen DP4, useful as
PT immunomodulators for treating e.g. tumors, based on inhibition of
PT binding.
XX
PS Disclosure; SEQ ID NO 10; 70pp; French.

The invention relates to a process for selecting ligands (A) of HLA (human leukocyte antigen)-DP4 comprising: (a) incubating purified DP4 with a labelled peptide (I) in presence of different concentrations of test compounds; (b) separating complexes formed; (c) determining DP4-(I) complexes by measuring a signal from the label; and (d) selecting compounds having binding IC50 less than 1000 nM, corresponding to the concentration required to inhibit 50 % binding of (I). (I) has signal-to-noise ratio over 5, at 10 nM, in a direct binding test to DP4. (A) cause activation of T cells, or their anergy. (A), or nucleic acid that encodes them, are useful as immunomodulators, including uses in vaccines against pathogens and tumor cells, also for treating autoimmune diseases (multiple sclerosis and type I diabetes), allergy and graft rejection. (A) are useful as reagents for diagnosing the immune status of an individual, while labelled complexes of DP4 with (A) are used to select antigen-specific CD4+ T cells. The method identifies ligands specific for HLA-DP4 and allows exact definition of the binding motif shared by DP4 binding ligands. This sequence represents an example of a peptide ligand of the invention. The peptides are labelled (biotinylated) at their N-terminal.

SEQ Sequence 20 AA;

Alignment Scores:

Pred. No.:	Length:
Score: 1.76e-09	20
Percent Similarity: 20.00	Matches: 20
Best Local Similarity: 100.00%	Conservative: 0
Query Match: 100.00%	Mismatches: 0
DB: 11.11%	Indels: 0
	Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x ADD71448 (1-20)

478 ATGTGGATCAGCCAGGCGTTTCGCCCGTGTTTGGCTGCAGCCCTCAGGGCAGAGG 537
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1 MettPlletmngIncyseheueProvalPheLevalGlnProProsergIyGlnary 20

RESULT 45
 AAY52435
 ID AAY52435 standard; protein; 18 AA.
 XX
 AC AAY52435;
 XX
 DT 15-FEB-2000 (first entry)
 XX
 DE Human tumour antigen NY-ESO-1 peptide #8.
 XX
 KW Cancer; tumour; antigen; MHC; major histocompatibility complex; Class II;
 KW T-cell; helper; stimulation; proliferation; treatment; diagnosis;
 KW prevention; melanoma; breast cancer; ovarian cancer; prostate cancer;
 KW hepatoma; thyroid cancer; bladder cancer; lung cancer; lymphoma.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN MO953938-A1.
 XX
 PD 28-OCT-1999.
 XX
 PF 24-MAR-1999; 99MO-US006875.
 XX
 PR 17-APR-1998; 98US-00062422.
 PR 02-OCT-1998; 98US-00165546.
 XX
 PA (LUDM-) LUDMIG INST CANCER RES.
 XX
 PI Stockert E, Jager E, Chen Y, Scanlan M, Alexander K, Old LJ;
 PI Gure A, Rittler G;
 XX
 DR WPI; 2000-038483/03.
 XX
 PT Novel peptides which bind to MHC class I and MHC class II molecules,
 PT useful for therapeutic and diagnostic purposes.
 XX
 PS Claim 4; Page 22; 49pp; English.
 XX
 CC Peptides #8-#13 (AAY52435-Y52440) are peptides derived from the human
 CC tumour antigen, NY-ESO-1 (AAY52430) which can bind to MHC (major
 CC histocompatibility Class II HLA-DR5) molecules, thereby stimulating
 CC proliferation of helper T-cells. CDNA encoding NY-ESO-1 was initially
 CC isolated from an oesophagus squamous cell cancer cDNA library. Tissue
 CC localisation studies revealed it to be expressed at high levels in normal
 CC ovary and testis but not in normal colon, kidney, liver, brain,
 CC oesophagus and skin. It was expressed in certain tumours and tumour cell
 CC lines with some degree of frequency - these included melanoma specimens
 CC and cell lines, and breast and bladder cancer specimens, with expression
 CC in other tumour types being sporadic. These NY-ESO-1-derived peptides may
 CC be used in methods and compositions used for the treatment, diagnosis and
 CC prevention of cancers (such as melanoma, breast cancer, prostate cancer,
 CC lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer, or
 CC lymphoma) and to stimulate the proliferation of T cells
 XX
 SQ Sequence 18 AA:
 Alignment Scores:
 Pred. No: 1,29e-07 Length: 18
 Score: 18.00 Matches: 18
 Percent Similarity: 100.00% Conservative: 0
 Best local Similarity: 100.00% Mismatches: 0
 Query Match: 10.00% Indels: 0
 DB: 3 Gaps: 0
 US-10-023-182-1_COPY_54_593 (1-540) x AAY52435 (1-18)
 QY GCTGCAGACACCGCCAACTGAGAGCTTCATTCAGCTCTCCAGACAGTT 468
 Db 1 AIdAIdAsPhIeIrGInLeuSInUeSeIrIleSeRySleuGInGInLeu 18

Wed Jul 21 11:16:04 2004

us-10-023-182-1_copy_54_593.oli.rag

Page 26

Search completed: July 19, 2004, 12:11:44
Job time : 71.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_p1ue_n2p model

Run on: July 19, 2004, 12:08:47 ; Search time 17 Seconds
(without alignments)
3279.768 Million cell updates/sec

Title: US-10-023-182-1_COPY_54_593

Perfect score: 180
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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 segs, 51625971 residues

Word size: 1

Total number of hits satisfying chosen parameters: 355124

Minimum DB seq length: 5
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

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-DB=Issued Patents AA -QMT=fastan -SUFFIX=ol1.ra1 -MINMATCH=0.1 -LOOPL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=45 -MODE=LOCAL
-OUTMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=5 -MAXLEN=50
-USER=US10023182 @cgn_1_1_33 @runat.19072004.125309.4330 -NCPU=6 -ICPU=3
-NO MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=150 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

Issued Patents AA: *
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2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*
3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*
4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/2/1aa/PCTUS.COMB.pep:*
6: /cgn2_6/ptodata/2/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
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2	18	10.0	18	3	US-09-359-503-9
3	18	10.0	18	3	US-09-359-503-10
4	18	10.0	18	3	US-09-359-503-11
5	18	10.0	18	3	US-09-359-503-12
6	18	10.0	18	3	US-09-359-503-13
7	11	6.1	11	3	US-09-183-931-42
8	11	6.1	11	3	US-09-359-503-4
9	11	6.1	11	3	US-09-062-422-4
10	11	6.1	11	3	US-08-937-263B-4
11	11	6.1	11	3	US-09-166-448-79
12	11	6.1	11	4	US-09-705-160-42

13	11	6.1	11	4	US-09-440-621-1	Sequence 1, Appl1
14	11	6.1	11	4	US-09-697-884-79	Sequence 79, Appl1
15	11	6.1	11	4	US-09-751-798-4	Sequence 4, Appl1
16	11	6.1	11	4	US-09-344-040C-130	Sequence 130, App
17	11	6.1	11	4	US-09-574-749B-33	Sequence 33, Appl1
18	11	6.1	11	4	US-09-676-005B-1	Sequence 1, Appl1
19	11	6.1	11	4	US-09-833-039A-130	Sequence 130, App
20	10	5.6	10	3	US-09-359-503-7	Sequence 7, Appl1
21	10	5.6	10	4	US-09-344-040C-126	Sequence 126, App
22	10	5.6	10	4	US-09-344-040C-127	Sequence 127, App
23	10	5.6	10	4	US-09-344-040C-128	Sequence 128, App
24	10	5.6	10	4	US-09-344-040C-129	Sequence 129, App
25	10	5.6	10	4	US-09-676-005B-11	Sequence 11, Appl1
26	10	5.6	10	4	US-09-833-039A-126	Sequence 126, App
27	10	5.6	10	4	US-09-833-039A-127	Sequence 127, App
28	10	5.6	10	4	US-09-833-039A-128	Sequence 128, App
29	10	5.6	10	4	US-09-833-039A-129	Sequence 129, App
30	9	5.0	9	3	US-09-183-931-43	Sequence 43, Appl1
31	9	5.0	9	3	US-09-183-931-44	Sequence 44, Appl1
32	9	5.0	9	3	US-09-359-503-5	Sequence 5, Appl1
33	9	5.0	9	3	US-09-359-503-6	Sequence 6, Appl1
34	9	5.0	9	3	US-09-062-422-5	Sequence 5, Appl1
35	9	5.0	9	3	US-09-062-422-6	Sequence 6, Appl1
36	9	5.0	9	3	US-08-937-263B-5	Sequence 5, Appl1
37	9	5.0	9	3	US-08-937-263B-6	Sequence 6, Appl1
38	9	5.0	9	3	US-09-166-448-80	Sequence 80, Appl1
39	9	5.0	9	3	US-09-166-448-81	Sequence 81, Appl1
40	9	5.0	9	4	US-09-705-160-43	Sequence 43, Appl1
41	9	5.0	9	4	US-09-705-160-44	Sequence 44, Appl1
42	9	5.0	9	4	US-09-440-621-2	Sequence 2, Appl1
43	9	5.0	9	4	US-09-440-621-3	Sequence 3, Appl1
44	9	5.0	9	4	US-09-697-884-80	Sequence 80, Appl1
45	9	5.0	9	4	US-09-697-884-81	Sequence 81, Appl1

ALIGNMENTS

RESULT 1
US-09-359-503-8
; Sequence 8, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, Alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359, 503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165, 546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062, 422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937, 263
; FILING DATE: September 15, 1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6251603man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS: 18 amino acids
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-359-503-8

Alignment Scores:
Pred. No.: 9,44e-09 Length: 18
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.00% Indels: 0
Gaps: 0
DB: 3

US-10-023-182-1_copy_54_593 (1-540) x US-09-359-503-8 (1-18)

QY 415 GCGGACGACCGCACTGCTTCATCAGCTCCTGCTCCAGCAGCTT 468
Db 1 AAlaAlaSpHisArgGlnLeuGlnIleuSerIleSerSerCysLeuGlnIleu 18

RESULT 2
US-09-359-503-9
Sequence 9, Application US/09359503
Patent No. 6251603
GENERAL INFORMATION:
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, Alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6251603man D.
REGISTRATION NUMBER: 30,946

to NY-

REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-359-503-9

Alignment Scores:
Pred. No.: 9,44e-09 Length: 18
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.00% Indels: 0
Gaps: 0
DB: 3

US-10-023-182-1_copy_54_593 (1-540) x US-09-359-503-9 (1-18)

QY 361 GTGCTTGAGAGGAGTTCAGCTGTCGCGCAACATGACTATCCGACT 414
Db 1 ValLeuLeuLysGlnPheThrValSerCysAsnIleuThrIleArgLeuThr 18

RESULT 3
US-09-359-503-10
Sequence 10, Application US/09359503
Patent No. 6251603
GENERAL INFORMATION:
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, Alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6251603man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:

to NY-1

LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-09-359-503-10

Alignment Scores:

Pred. No.:	9.44e-09	Length:	18
Score:	18.00	Matches:	18
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	10.00%	Indels:	0
DB:	3	Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-359-503-10 (1-18)

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|||||
Db 1 ProleuprovalProglyvalleuvalleuvalsgluPheHtrValSergGlyAsnIle 18

RESULT 4

US-09-359-503-11
Sequence 11, Application US/09359503
Patent No. 6251603

GENERAL INFORMATION:
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, Alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESS: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6251603man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear

to NY-

Pred. No.:	9.44e-09	Length:	18
Score:	18.00	Matches:	18
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	10.00%	Indels:	0
DB:	3	Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-359-503-11 (1-18)

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Db 1 GlyAlaIaSerGlyLeuAsnGlyCysCySerGcysIyAlaArgIyProGlu 18

RESULT 5

US-09-359-503-12
Sequence 12, Application US/09359503
Patent No. 6251603

GENERAL INFORMATION:
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, Alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESS: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6251603man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-09-359-503-12

Alignment Scores:

Pred. No.:	9.44e-09	Length:	18
Score:	18.00	Matches:	18
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	10.00%	Indels:	0
DB:	3	Gaps:	0

Alignment Scores:

to NY-I

US-10-023-182-1_COPY_54_593 (1-540) x US-09-359-503-12 (1-18)
QY 253 ACCCGCTCTGAGTTCTACCTGCGCATGCTTTGCGACAGCCATGAGCA 306
DB 1 SerArgLeuGluGlnPheTyrLeuAlaMetProPheAlaThrProMetGlnAla 18
RESULT 6
US-09-359-503-13
Sequence 13, Application US/09359503
Patent No. 6251603
GENERAL INFORMATION:
APPLICANT: Jager, Elke, Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, Alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6251603man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-359-503-13
Alignment Scores:
Pred. No.: 9,44e-09 Length: 18
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.00% Indels: 0
DB: 3 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x US-09-359-503-13 (1-18)
QY 379 ACTGTTCCGAGACATAGTACTGACGACGAGCTGCGACAGCCAGCA 432
DB 1 ThrValSerGlyAsnIleuThrIleArgLeuThrAlaAlaAspHisArgGln 18

US-09-183-931-42
RESULT 7
US-09-183-931-42
Sequence 42, Application US/09183931C
Patent No. 6210886
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Brasseur, Francis
APPLICANT: Boon-Fallier, Thierry
TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
FILE REFERENCE: LUD 5527.1-JEL/RS
CURRENT APPLICATION NUMBER: US/09/183,931C
CURRENT FILING DATE: 2000-02-28
EARLIER APPLICATION NUMBER: US 09/018,422
EARLIER FILING DATE: 1998 - 02 - 04
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 42
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION:
US-09-183-931-42
Alignment Scores:
Pred. No.: 0.0461 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 3 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x US-09-183-931-42 (1-11)
QY 469 TCCCTGTGATGTGATACCGCATGCTTTCTG 501
DB 1 SerLeuMetIleThrGlnCysPheLeu 11
RESULT 8
US-09-359-503-4
Sequence 4, Application US/09359503
Patent No. 6251603
GENERAL INFORMATION:
APPLICANT: Jager, Elke, Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, Alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:

to NY-1

APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6251603man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-359-503-4

Alignment Scores:
Pred. No.: 0.0461 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 3 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-359-503-4 (1-11)

QY 469 TCCTGTGATGTGATCAGCAGTGTCTTG 501
DB 1 SerleuNeuMetTryPleThcInCysPheLeu 11

RESULT 9
US-09-062-422-4
Sequence 4, Application US/09062422
Patent No. 6252052
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
TITLE OF INVENTION: THEREFROM
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,422
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6252052man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-062-422-4

Alignment Scores:
Pred. No.: 0.0461 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 3 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-062-422-4 (1-11)

QY 469 TCCTGTGATGTGATCAGCAGTGTCTTG 501
DB 1 SerleuNeuMetTryPleThcInCysPheLeu 11

RESULT 10
US-08-937-263B-4
Sequence 4, Application US/08937263B
Patent No. 6274145
GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander, Knuth; Drifflout, Jan W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
TITLE OF INVENTION: ITSELF, AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Sinn, Eric; Patent Agent
REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-937-263B-4

Alignment Scores:
Pred. No.: 0.0461 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0

DB: 3 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x US-08-937-263B-4 (1-11)
QY 469 TCCTGTGATGTGATCAGCAGTCTTCTG 501
DB 1 SerLeuMetTPrIleThrGlnCysPheLeu 11
RESULT 11
US-09-166-448-79
; Sequence 79, Application US/09166448
; Patent No. 6291430
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vantomme, Valérie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/166,448
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-448-79
Alignment Scores:
Pred. No.: 0.0461 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 3 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x US-09-166-448-79 (1-11)
QY 469 TCCTGTGATGTGATCAGCAGTCTTCTG 501
DB 1 SerLeuMetTPrIleThrGlnCysPheLeu 11
RESULT 12
US-09-705-160-42
; Sequence 42, Application US/09705160
; Patent No. 6387630
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; FILE REFERENCE: LUD 5527.3-JEL/MAS
; CURRENT APPLICATION NUMBER: US/09/705,160
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 09/183,931
; PRIOR FILING DATE: 1998 - 10 - 30
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 42
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-705-160-42
Alignment Scores:
Pred. No.: 0.0461 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 3 Gaps: 0

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 4 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x US-09-705-160-42 (1-11)
QY 469 TCCTGTGATGTGATCAGCAGTCTTCTG 501
DB 1 SerLeuMetTPrIleThrGlnCysPheLeu 11
RESULT 13
US-09-440-621-1
; Sequence 1, Application US/09440621
; Patent No. 6417165
; GENERAL INFORMATION:
; APPLICANT: Valmori, Danila
; APPLICANT: Cerottini, Jean-Charles
; APPLICANT: Romero, Pedro
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629
; CURRENT APPLICATION NUMBER: US/09/440,621
; CURRENT FILING DATE: 1998-11-15
; EARLIER APPLICATION NUMBER: US 09/165,546
; EARLIER FILING DATE: 1998-10-02
; EARLIER APPLICATION NUMBER: US 09/062,422
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: US 08/725,162
; EARLIER FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 1
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-440-621-1
Alignment Scores:
Pred. No.: 0.0461 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 4 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x US-09-440-621-1 (1-11)
QY 469 TCCTGTGATGTGATCAGCAGTCTTCTG 501
DB 1 SerLeuMetTPrIleThrGlnCysPheLeu 11
RESULT 14
US-09-697-884-79
; Sequence 79, Application US/09697884
; Patent No. 6426217
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vantomme, Valérie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/697,884
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 79
; LENGTH: 11

TYPE: PRF
ORGANISM: Homo sapiens
US-09-697-884-79

Alignment Scores:
Pred. No.: 0.0461 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-697-884-79 (1-11)

QY 469 TCCTGTGATGATCGACGACGCTTTCTG 501
Db 1 Serleuueuettptlertnrglncysphelu 11

RESULT 15
US-09-751-798-4
Sequence 4, Application US/09751798
Patent No. 6525177

GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 652517man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-751-798-4

Alignment Scores:
Pred. No.: 0.0461 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-751-798-4 (1-11)

QY 469 TCCTGTGATGATCGACGACGCTTTCTG 501
Db 1 Serleuueuettptlertnrglncysphelu 11

RESULT 16
US-09-344-040C-130
Sequence 130, Application US/09344040C
Patent No. 6548064

GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfeundschnur, Michael
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determini
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
TITLE OF INVENTION: Gene, and Uses Thereof
FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 130
LENGTH: 11
TYPE: PRF
ORGANISM: Homo sapiens
US-09-344-040C-130

Alignment Scores:
Pred. No.: 0.0461 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-344-040C-130 (1-11)

QY 469 TCCTGTGATGATCGACGACGCTTTCTG 501
Db 1 Serleuueuettptlertnrglncysphelu 11

RESULT 17
US-09-574-749B-33
Sequence 33, Application US/09574749B
Patent No. 6548299

GENERAL INFORMATION:
APPLICANT: ROSENZWEIG, Michael
APPLICANT: PYKETT, Mark J.
APPLICANT: SCADDEN, David T.
APPLICANT: POZNAISKY, Mark C.
TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
FILE REFERENCE: C1005/7012/KA/ERG
CURRENT APPLICATION NUMBER: US/09/574,749B
CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US 60/107,972
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: PCT/US99/26795
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 09/524,749
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 11

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/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Homo Sapiens source
US-09-574-749B-33

Alignment Scores:
Pred. No.: 0.0461 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-574-749B-33 (1-11)
QY 469 TCCCTGTGATGATCAGCAGAGTCTTCTG 501
DB 1 SerLeuLeuMetTrpIleThrgInCysPheLeu 11

RESULT 18
US-09-676-005B-1
/ Sequence 1, Application US/09676005B
/ Patent No. 6605711
/ GENERAL INFORMATION:
/ APPLICANT: Valmori, Danila
/ APPLICANT: Cerrotini, Jean, Charels
/ APPLICANT: Romero, Pedro
/ TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
/ FILE REFERENCE: LUD 5629.2
/ CURRENT APPLICATION NUMBER: US/09/676, 005B
/ PRIOR FILING DATE: 2000-09-29
/ PRIOR APPLICATION NUMBER: US09/514, 036
/ PRIOR FILING DATE: 2000-02-05
/ PRIOR APPLICATION NUMBER: US09/440, 621
/ PRIOR FILING DATE: 1999-11-15
/ PRIOR APPLICATION NUMBER: US 09/165, 546
/ PRIOR FILING DATE: 1998-10-02
/ PRIOR APPLICATION NUMBER: US 09/062, 422
/ PRIOR FILING DATE: 1998-04-17
/ PRIOR APPLICATION NUMBER: US 08/725, 162
/ PRIOR FILING DATE: 1996-10-03
/ NUMBER OF SEQ ID NOS: 27
/ SEQ ID NO 1
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
US-09-676-005B-1

Alignment Scores:
Pred. No.: 0.0461 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-676-005B-1 (1-11)
QY 469 TCCCTGTGATGATCAGCAGAGTCTTCTG 501
DB 1 SerLeuLeuMetTrpIleThrgInCysPheLeu 11

RESULT 19
US-09-833-039A-130
/ Sequence 130, Application US/09833039A
/ Patent No. 6673350
/ GENERAL INFORMATION:
/ APPLICANT: Tureci, Ozlem
/ APPLICANT: Sahin, Ugur
/ APPLICANT: Pfreundschuh, Michael
/ TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
```

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/ FILE REFERENCE: LUD 5622.1
/ CURRENT APPLICATION NUMBER: US/09/833, 039A
/ CURRENT FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: US 09/409, 455
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: US 09/344, 040
/ PRIOR FILING DATE: 1999-06-26
/ PRIOR APPLICATION NUMBER: US 09/105, 839
/ PRIOR FILING DATE: 1998-06-26
/ NUMBER OF SEQ ID NOS: 131
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 130
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-833-039A-130

Alignment Scores:
Pred. No.: 0.0461 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-833-039A-130 (1-11)
QY 469 TCCCTGTGATGATCAGCAGAGTCTTCTG 501
DB 1 SerLeuLeuMetTrpIleThrgInCysPheLeu 11

RESULT 20
US-09-359-503-7
/ Sequence 7, Application US/09359503
/ Patent No. 6251603
/ GENERAL INFORMATION:
/ APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
/ APPLICANT: Knuth, Alexander
/ TITLE OF INVENTION: Method for Determining Status of A
/ TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
/ NUMBER OF SEQUENCES: 14
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fulbright & Jaworski, L.L.P.
/ STREET: 666 Fifth Avenue
/ CITY: New York City
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10103
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
/ COMPUTER: IBM
/ OPERATING SYSTEM: PC-DOS
/ SOFTWARE: WordPerfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/359, 503
/ FILING DATE: July 23, 1999
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/165, 546
/ FILING DATE: October 2, 1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/062, 422
/ FILING DATE: April 17, 1998
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 09/937, 263
/ FILING DATE: September 15, 1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 08/752, 182
/ FILING DATE: 03-October-1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Hanson, No. 6251603man D.
/ REGISTRATION NUMBER: 30,946
```

```
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-359-503-7

Alignment Scores:
Pred. No.: 0.417 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56% Indels: 0
DB: 3 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-359-503-7 (1-10)

Cy 472 CTGTTGATGATCAGCAGTCTTCTG 501
Db 1 LeuLeuWettrPileThrgInGInGySheLeu 10

RESULT 21
US-09-344-040C-126
Sequence 126, Application US/09344040C
Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
FILE OF INVENTION: Gene, and Uses Thereof
FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 126
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-344-040C-126

Alignment Scores:
Pred. No.: 0.417 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-344-040C-126 (1-10)

Cy 115 GCCACGGCGGAGAGTCCCGGGCGCA 144
Db 1 AlaThrgIlyGlyAlrgGlyProArGlyAla 10

RESULT 22
US-09-344-040C-127
Sequence 127, Application US/09344040C
Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
```

```
APPLICANT: Pfreundschuh, Michael
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
FILE OF INVENTION: Gene, and Uses Thereof
FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 127
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-344-040C-127

Alignment Scores:
Pred. No.: 0.417 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-344-040C-127 (1-10)

Cy 175 GCGCGCGCGGGGTCCGATGGCGGCG 204
Db 1 GlyAlaProArGlyProHISgIyGlyAla 10

RESULT 23
US-09-344-040C-128
Sequence 128, Application US/09344040C
Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
FILE OF INVENTION: Gene, and Uses Thereof
FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 128
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-344-040C-128

Alignment Scores:
Pred. No.: 0.417 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-344-040C-128 (1-10)

Cy 310 CTGGCCGCGAGAGCTGGCCAGATGCC 339
```

```
Db      1 LeuAlaArgArgSerLeuAlaGlnAspAla 10
RESULT 24
US-09-344-040C-129
; Sequence 129, Application US/09344040C
; Patent No. 6548054
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stenvanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 129
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-129

Alignment Scores:
Pred. No.:      0.417      Length:      10
Score:          10.00      Matches:      10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    5.56%      Indels:      0
DB:             4          Gaps:          0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-344-040C-129 (1-10)
Qy      484 ATCAGCAGTGGCTTCTGCGCGTGTGTTT 513
Db      1 lIeThrGlnCySPhenLeuProValPheLeu 10
RESULT 25
US-09-676-005B-11
; Sequence 11, Application US/09676005B
; Patent No. 6605711
; GENERAL INFORMATION:
; APPLICANT: Valmori, Daniela
; APPLICANT: Cerrotini, Jean, Charels
; APPLICANT: Romero, Pedro
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629.2
; CURRENT APPLICATION NUMBER: US/09/676,005B
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US09/514,036
; PRIOR FILING DATE: 2000-02-05
; PRIOR APPLICATION NUMBER: US09/440,621
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 09/165,546
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: US 09/062,422
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 08/725,162
; PRIOR FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 11
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-676-005B-11
```

```
Alignment Scores:
Pred. No.:      0.417      Length:      10
Score:          10.00      Matches:      10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    5.56%      Indels:      0
DB:             4          Gaps:          0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-676-005B-11 (1-10)
Qy      469 TCCGTTGATGTGATCAGCAGTGGCTTT 498
Db      1 SerLeuMetIleTlrPheGlnCysPhe 10
RESULT 26
US-09-833-039A-126
; Sequence 126, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-126

Alignment Scores:
Pred. No.:      0.417      Length:      10
Score:          10.00      Matches:      10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    5.56%      Indels:      0
DB:             4          Gaps:          0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-833-039A-126 (1-10)
Qy      115 GCCACGGGCGGCGAGAGTCCCGGGGCGCA 144
Db      1 AlaThrGlyGlyArgGlyProArgGlyAla 10
RESULT 27
US-09-833-039A-127
; Sequence 127, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 127
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-127

Alignment Scores:
Pred. No.:      0.417      Length:      10
Score:          10.00      Matches:      10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    5.56%      Indels:      0
DB:             4          Gaps:          0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-833-039A-127 (1-10)

QY      175 GAGCGCCGCGGAGTCCGATGCGCGCG 204
DB      1 GlyAlaProArgGlyProHisGlyGlyAla 10

RESULT 28
US-09-833-039A-128
; Sequence 128, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 128
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-128

Alignment Scores:
Pred. No.:      0.417      Length:      10
Score:          10.00      Matches:      10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    5.56%      Indels:      0
DB:             4          Gaps:          0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-833-039A-128 (1-10)

QY      310 CTGCGCCGAGAGCTGCGCCGAGATGCC 339
DB      1 LeuAlaArgSerLeuAlaGlnAspAla 10

RESULT 29
US-09-833-039A-129
; Sequence 129, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
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; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 129
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-129

Alignment Scores:
Pred. No.:      0.417      Length:      10
Score:          10.00      Matches:      10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    5.56%      Indels:      0
DB:             4          Gaps:          0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-833-039A-129 (1-10)

QY      484 ATCAGCAGTGTCTTCTGCCCGTGTG 513
DB      1 IleThrGlnCysPheLeuProValPheLeu 10

RESULT 30
US-09-183-931-43
; Sequence 43, Application US/09183931C
; Patent No. 6210886
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Fallieur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
; FILE REFERENCE: LUD 5527.1-JEL/ES
; CURRENT APPLICATION NUMBER: US/09/183,931C
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: US 09/018,422
; EARLIER FILING DATE: 1998 - 02 - 04
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-183-931-43

Alignment Scores:
Pred. No.:      1.13e+07      Length:      9
Score:          9.00          Matches:      9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    5.00%      Indels:      0
DB:             3          Gaps:          0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-183-931-43 (1-9)

QY      469 TCCTCTGTGATGATGATCAGCAGTGC 495
DB      1 SerLeuLeuMetTrpIleThrGlnCys 9

RESULT 31
US-09-183-931-44
; Sequence 44, Application US/09183931C
; Patent No. 6210886
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
```

APPLICANT: Boon-Falleur, Thierry
TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
FILE REFERENCE: LUD 5527.1-JEL/ES
CURRENT APPLICATION NUMBER: US/09/183,931C
CURRENT FILING DATE: 2000-02-28
EARLIER APPLICATION NUMBER: US 09/018,422
EARLIER FILING DATE: 1998 - 02 - 04
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 44
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION:
US-09-183-931-44

Alignment Scores:
Pred. No.: 1.13e+07 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 3 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-183-931-44 (1-9)

QY 463 CAGCTTCCCGTGTGATCAGTCACG 489
DB 1 GlnLeuSerLeuLeuMetTrpIleThrGlnCys 9

RESULT 32
US-09-359-503-5
Sequence 5, Application US/09359503
Patent No. 6251603
GENERAL INFORMATION:
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, Alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6251603man D.
REGISTRATION NUMBER: 30,946

to NY-

REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-359-503-5

Alignment Scores:
Pred. No.: 1.13e+07 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 3 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-359-503-5 (1-9)

QY 469 TCCGCTGTGATGATCAGTCACGTCG 495
DB 1 SerLeuLeuMetTrpIleThrGlnCys 9

RESULT 33
US-09-359-503-6
Sequence 6, Application US/09359503
Patent No. 6251603
GENERAL INFORMATION:
APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
APPLICANT: Knuth, Alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESS: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6251603man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

to NY-1

US-08-937-263B-5
; Sequence 5, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drifhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/937,263B
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Simm, Eric, Patent Agent
; REGISTRATION NUMBER: 40,177
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-937-263B-5

Alignment Scores:
Pred. No.: 1.13e+07 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 3 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-08-937-263B-5 (1-9)
QY 469 TCCCTTGATGATGATCGCAGTCG 495
DB 1 SerLeuLeuMetIrpIleThraIncyS 9

RESULT 37
US-08-937-263B-6
; Sequence 6, Application US/08937263B
; Patent No. 6274145
; GENERAL INFORMATION:
; APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
; APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
; APPLICANT: Alexander, Knuth; Drifhout, Jan W.
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
; TITLE OF INVENTION: ITSELF, AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSES: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City

STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/937,263B
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Simm, Eric, Patent Agent
REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-937-263B-6

Alignment Scores:
Pred. No.: 1.13e+07 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 3 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-08-937-263B-6 (1-9)
QY 463 CAGCTTCCCTTGATGATGATCAGC 489
DB 1 GinLeuSerLeuLeuMetIrpIleThr 9

RESULT 38
US-09-166-448-80
; Sequence 80, Application US/09166448
; Patent No. 6291430
; GENERAL INFORMATION:
; APPLICANT: Chauv, Pascal
; APPLICANT: Vantomme, Valerie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corbals, Jurgen
; TITLE OF INVENTION: MAGB-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/166,448
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-448-80

Alignment Scores:
Pred. No.: 1.13e+07 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 3 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-166-448-80 (1-9)

Oy 469 TCCCGTGTGATGCACGACGTC 495

Db 1 SerleuSeuMetTpiLeuThGlnCys 9

RESULT 39

US-09-166-448-81

; Sequence 81, Application US/09166448

; Patent No. 6291430

; GENERAL INFORMATION:

; APPLICANT: Chau, Pascal

; APPLICANT: Vantomme, Valrie

; APPLICANT: Stroobant, Vincent

; APPLICANT: Boon-Falleur, Thierry

; APPLICANT: Thielemans, Kris

; APPLICANT: van der Bruggen, Pierre

; APPLICANT: Cortbals, Jurgen

; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS

; FILE REFERENCE: L0461/7052

; CURRENT APPLICATION NUMBER: US/09/166,448

; CURRENT FILING DATE: 1998-10-05

; NUMBER OF SEQ ID NOS: 81

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 81

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-166-448-81

Alignment Scores:

Pred. No.: 1.13e+07 Length: 9

Score: 9.00 Matches: 9

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 5.00% Indels: 0

DB: 3 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-166-448-81 (1-9)

Oy 463 CAGCTTCCCTGTGATGCATGCACG 489

Db 1 GlnSeuSerLeuSeuMetTpiLeuThr 9

RESULT 40

US-09-705-160-43

; Sequence 43, Application US/09705160

; Patent No. 6387630

; GENERAL INFORMATION:

; APPLICANT: Van Baren, Nicolas

; APPLICANT: Brasseur, Francis

; APPLICANT: Boon-Falleur, Thierry

; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING

; FILE REFERENCE: LUD 5527.3-JEL/MAS

; CURRENT APPLICATION NUMBER: US/09/705,160

; CURRENT FILING DATE: 2001-11-02

; PRIOR APPLICATION NUMBER: US 09/183,931

; PRIOR FILING DATE: 1998 - 10 - 30

; NUMBER OF SEQ ID NOS: 44

; SEQ ID NO 43

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION:

; US-09-705-160-43

Alignment Scores:

Pred. No.: 1.13e+07 Length: 9

Score: 9.00 Matches: 9

Percent Similarity: 100.00% Mismatches: 0

Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 5.00% Indels: 0

DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-705-160-43 (1-9)

Oy 469 TCCCGTGTGATGCATGCACGACGTC 495

Db 1 SerleuSeuMetTpiLeuThGlnCys 9

RESULT 41

US-09-705-160-44

; Sequence 44, Application US/09705160

; Patent No. 6387630

; GENERAL INFORMATION:

; APPLICANT: Van Baren, Nicolas

; APPLICANT: Brasseur, Francis

; APPLICANT: Boon-Falleur, Thierry

; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING

; FILE REFERENCE: LUD 5527.3-JEL/MAS

; CURRENT APPLICATION NUMBER: US/09/705,160

; CURRENT FILING DATE: 2001-11-02

; PRIOR APPLICATION NUMBER: US 09/183,931

; PRIOR FILING DATE: 1998 - 10 - 30

; NUMBER OF SEQ ID NOS: 44

; SEQ ID NO 44

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; OTHER INFORMATION:

; US-09-705-160-44

Alignment Scores:

Pred. No.: 1.13e+07 Length: 9

Score: 9.00 Matches: 9

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 5.00% Indels: 0

DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-705-160-44 (1-9)

Oy 463 CAGCTTCCCTGTGATGCATGCACG 489

Db 1 GlnSeuSerLeuSeuMetTpiLeuThr 9

RESULT 42

US-09-440-621-2

; Sequence 2, Application US/09440621

; Patent No. 6417165

; GENERAL INFORMATION:

; APPLICANT: Valmori, Danila

; APPLICANT: Cerottini, Jean-Charles

; APPLICANT: Romero, Pedro

; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof

; FILE REFERENCE: LUD 5629

; CURRENT APPLICATION NUMBER: US/09/440,621

; CURRENT FILING DATE: 1999-11-15

; EARLIER APPLICATION NUMBER: US 09/165,546

; EARLIER FILING DATE: 1998-10-02

; EARLIER APPLICATION NUMBER: US 09/062,422

; EARLIER FILING DATE: 1998-04-17

; EARLIER APPLICATION NUMBER: US 08/725,162

; EARLIER FILING DATE: 1996-10-03

; NUMBER OF SEQ ID NOS: 10

; SEQ ID NO 2

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; US-09-440-621-2

Alignment Scores:
Pred. No.: 1.13e+07 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-440-621-2 (1-9)

QY 469 TCCTTGTGATGATCGACGACGTC 495
DB 1 SerLeuMettripleThrGlnCys 9

RESULT 43
US-09-440-621-3
; Sequence 3, Application US/09440621
; Patent No. 6417165
; GENERAL INFORMATION:
; APPLICANT: Valmorl, Danila
; APPLICANT: Cerottini, Jean-Charles
; APPLICANT: Romero, Pedro
; TITLE OF INVENTION: Derivatives of NY-ESO-1 peptides and uses thereof
; FILE REFERENCE: LUD 5629
; CURRENT APPLICATION NUMBER: US/09/440,621
; EARLIER FILING DATE: 1999-11-15
; EARLIER APPLICATION NUMBER: US 09/165,546
; EARLIER FILING DATE: 1998-10-02
; EARLIER APPLICATION NUMBER: US 09/062,422
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: US 08/725,162
; EARLIER FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-440-621-3

Alignment Scores:
Pred. No.: 1.13e+07 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-440-621-3 (1-9)

QY 463 GAGCTTCCTGTTGATGATCGACG 489
DB 1 GlnLeuSerLeuMettripleThr 9

RESULT 44
US-09-697-884-80
; Sequence 80, Application US/09697884
; Patent No. 6426217
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vanlomme, Val,rie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Cortals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/697,884
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 09/166,448
; PRIOR FILING DATE: 1998-10-05

; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-697-884-80

Alignment Scores:
Pred. No.: 1.13e+07 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-697-884-80 (1-9)

QY 469 TCCTTGTGATGATCGACGACGTC 495
DB 1 SerLeuMettripleThrGlnCys 9

RESULT 45
US-09-697-884-81
; Sequence 81, Application US/09697884
; Patent No. 6426217
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vanlomme, Val,rie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Cortals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/697,884
; CURRENT FILING DATE: 2000-10-27
; PRIOR APPLICATION NUMBER: 09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-697-884-81

Alignment Scores:
Pred. No.: 1.13e+07 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-697-884-81 (1-9)

QY 463 GAGCTTCCTGTTGATGATCGACG 489
DB 1 GlnLeuSerLeuMettripleThr 9

Search completed: July 19, 2004, 12:13:19
Job time : 18 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - protein search, using frame_plus_nzp model

Run on: July 19, 2004, 12:13:16 ; Search time 44 Seconds
(without alignments)
7671.943 Million cell updates/sec

Title: US-10-023-182-1_COPY_54_593

Perfect score: 180
Sequence: 1 ATGCAGGCCGAGGCGCGG.....CTCCCTCAGGCGAGGCGCGC 540

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
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Searched: 1285345 seqs, 312560633 residues

Word size: 1

Total number of hits satisfying chosen parameters: 612412

Minimum DB seq length: 5
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Command line parameters:

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-O=/cgn2_1/USPTO_epool_p/US10023182/runat_19072004_125309_4360/app_query.fasta.1.711
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-LOOCL=0 -LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=011go
-TRANS=human40.cdi -LIST=45 -DICALIGN=200 -THR SCORE=quality -THR MIN=1
-ALIGN=45 -MODL=LOCAL -OUTFMT=ps -NORM=ext -HEARSIZE=500 -MINLEN=5 -MAXLEN=50
-USER=US10023182@cgn2_1_1130@runat_19072004_125309_4360 -NCPU=6 -ICPU=3
-NO_MMAP -LARGESQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : Published Applications_AA:*

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15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
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18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No. Score Query Match Length DB ID Description

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16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7	16.7
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US-10-296-734-1400	US-10-296-734-1402	US-10-296-734-1404	US-10-296-734-1406	US-10-296-734-1408	US-10-296-734-1410	US-10-296-734-1412	US-10-296-734-1414	US-10-296-734-1416	US-10-296-734-1418	US-10-296-734-1420	US-10-296-734-1422	US-10-296-734-1424	US-10-296-734-1426	US-10-296-734-1428	US-10-296-734-1430	US-10-296-734-1432	US-10-296-734-1434	US-10-296-734-1436	US-10-296-734-1438	US-10-296-734-1440	US-10-296-734-1442	US-10-296-734-1444	US-10-296-734-1446	US-10-296-734-1448	US-10-296-734-1450	US-10-296-734-1452	US-10-296-734-1454	US-10-296-734-1456	US-10-296-734-1458	US-10-296-734-1460	US-10-296-734-1462	US-10-296-734-1464	US-10-296-734-1466	US-10-296-734-1468	US-10-296-734-1470	US-10-296-734-1472	US-10-296-734-1474	US-10-296-734-1476	US-10-296-734-1478	US-10-296-734-1480	US-10-296-734-1482	US-10-296-734-1484	US-10-296-734-1486	US-10-296-734-1488	US-10-296-734-1490		
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ALIGNMENTS

RESULT 1
US-10-296-734-1400
; Sequence 1400, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296, 734
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1400
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 2
US-10-296-734-1400

Alignment Scores:


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DB: 12 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x US-10-296-734-1414 (1-30)
QY 355 CCAGGGGCTCTGTGAGGAGTTCACTGTCGGGCAACATCTAGACTATCCGACTGCT 414
DB 1 ProGlyValLeuLeuLysGlnPheThrValSerGlyAsnIleLeuThrIleArgLeuThr 20
QY 415 GCTGCAGACACCGCCCAACTGCAGCTCTCC 444
DB 21 AlaAlaAspHisArgGlnLeuGlnLeuSer 30
RESULT 9
US-10-296-734-1416
; Sequence 1416, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1416
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 10
US-10-296-734-1416
Alignment Scores:
Pred. No.: 3,3e-17 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 12 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x US-10-296-734-1416 (1-30)
QY 400 ACTATCCGACTGCTGCTGAGCAGCCGCAACTGCACTCTCCATGCTGCTGCTC 459
DB 1 ThrIleArgLeuThrAlaAlaAspHisArgGlnLeuGlnLeuSerIleSerCysLeu 20
QY 460 CAGCAGCTTCCCTGTTGATGTGATCAGC 489
DB 21 GlnGlnLeuSerLeuLeuMetTrpIleThr 30
RESULT 10
US-10-296-734-1418
; Sequence 1418, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1418
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 11
US-10-296-734-1418
Alignment Scores:
Pred. No.: 3,3e-17 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 12 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x US-10-296-734-1418 (1-30)
QY 445 ATCAGCTCTGTGCTCCAGCAGCTTTCCTGTGATGTGATCAGCAGAGTCTTTCGCC 504
DB 1 IleSerSerCysLeuGlnGlnLeuSerLeuLeuMetTrpIleThrGlnCysPheLeuPro 20
QY 505 GTGTTTGGCTCAGCCTCCCTCAGGGCAG 534
DB 21 ValPheLeuAlaGlnProProSerGlyGln 30
RESULT 11
US-10-296-734-1424
; Sequence 1424, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1424
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 2
US-10-296-734-1424
Alignment Scores:
Pred. No.: 3,3e-17 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 12 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x US-10-296-734-1424 (1-30)
QY 80 CAGGGGGCAATGCTGGCGGCGCCAGAGAGCGGGTGCCAGCGGCGGAGAGTCTCCCGGG 139
DB 1 GlnGlyAlaMetLeuAlaAlaGlnGlnIleArgValProArgAlaAlaGlnValProGly 20
QY 140 GCGCAGGGGCGCAGCAGGGCTCCGGGGCCGG 169
DB 21 AlaGlnGlyGlnGlnGlyProArgGlyArg 30
RESULT 12
US-10-296-734-1426
; Sequence 1426, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
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; PRIOR APPLICATION NUMBER: AU P0761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1426
; LENGTH: 30
; TYPE: PRF
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLB segment 3
US-10-296-734-1426

Alignment Scores:
Pred. No.: 3,3e-17 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 12 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-296-734-1426 (1-30)

QY 125 GCAGAGGTCCTCCGCGGCGCAGAGGCGCAAGGCTCTCGGGCCGGAGAGAGCGCCCGC 184
DB 1 ALaGluValProGlyAlaGlnGlyGlnGlnGlyProArgGlyArgGluGlnAlaProArg 20

QY 185 GGGGTCCGCATGGCGGCGCGGCTTCAGGCG 214
DB 21 GlyValArgMetAlaAlaArgLeuGlnGly 30

RESULT 13
US-10-296-734-1432
; Sequence 1432, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savline
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P0761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1432
; LENGTH: 30
; TYPE: PRF
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: LAGE1 segment 2
US-10-296-734-1432

Alignment Scores:
Pred. No.: 3,3e-17 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 12 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-296-734-1432 (1-30)

QY 40 GATGCTGATGCGCCCAAGAGAGCCCTGGCATTCGTGATGATGCCAAGAGGCGCAATGCTGGCGGC 99
DB 1 AepAlaAepGlyProGlyGlyProGlyIleProAepGlyProGlyIleAepAlaGlyGly 20

QY 100 CCAGAGAGCGCGGGTGCCACGGGCGGCAGA 129
DB 21 ProGlyGluAlaGlyAlaThrGlyGlyArg 30

RESULT 14
US-10-364-614-16

```

```

: Sequence 16 Application US/10364614
: Publication No. US20030175250A1
: GENERAL INFORMATION:
: APPLICANT: JAGER, Elke
: APPLICANT: KNUTH, Alexander
: APPLICANT: OLD, Lloyd
: APPLICANT: Gnjatic, Sacha
: TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
: FILE REFERENCE: LUD 5726.1 CIP
: CURRENT APPLICATION NUMBER: US/10/364, 614
: CURRENT FILING DATE: 2003-02-24
: PRIOR APPLICATION NUMBER: US 60/355, 828
: PRIOR FILING DATE: 2002-02-13
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 16
: LENGTH: 30
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-364-614-16

Alignment Scores:
Pred. No.: 3,3e-17 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 14 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-364-614-16 (1-30)

Oy 238 GCCAGGGGGCCGGAGAGCCGCCCTTGCTTACTCGCCATGCTTTGGGACACCC 297
Db 1 AAlarGtlyProGlnSerArgLeuGluPheTyrLeuAlaMetProPheAlaThrPro 20
Oy 298 ATGAGCAGACGCTGCGCCCGCAGAGCGCTG 327
Db 21 MetGluAlaGluLeuAlaArgSerLeu 30

RESULT 15
US-10-296-734-1422
: Sequence 1422, Application US/10296734
: Publication No. US20040054137A1
: GENERAL INFORMATION:
: APPLICANT: Thompson, Scott A
: APPLICANT: Ramshaw, Ian A
: TITLE OF INVENTION: Synthetic molecules and uses therefor
: FILE REFERENCE: Savine
: CURRENT APPLICATION NUMBER: US/10/296, 734
: CURRENT FILING DATE: 2003-08-04
: PRIOR APPLICATION NUMBER: AU PQ7761/00
: PRIOR FILING DATE: 2000-05-26
: NUMBER OF SEQ ID NOS: 1507
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 1422
: LENGTH: 30
: TYPE: PRT
: ORGANISM: Artificial
: FEATURE:
: OTHER INFORMATION: NYS01b segment 1
US-10-296-734-1422

Alignment Scores:
Pred. No.: 2,45e-16 Length: 30
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.11% Indels: 0
DB: 12 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-296-734-1422 (1-30)
38 GCATGCTGATGAGCCGACGAGGCGCTTGACATTCCTGATGAGCCGACGAGGCGCATGCTGGCG 97

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Db 2 AlawetleuMetAlaGlnGlnAlaLeuAlaPheleuMetAlaGlnGlyAlaMetleuAla 21
QY 98 GCCCAGAGAGGGGGTGCACGGCG 124
Db 22 AlaGlnGlnAlaGArgValPProAla 30
RESULT 16
US-10-296-734-1448
; Sequence 1448, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1448
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; OTHER INFORMATION: LAGE1 segment 10
US-10-296-734-1448
Alignment Scores:
Pred. No.: 2,45e-16 Length: 30
Score: 29.00 Matches: 29
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.11% Indels: 0
DB: 12 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x US-10-296-734-1448 (1-30)
QY 403 ATCCGACTGCTGCTGCACGACCGCCGACGCTTCATCAGCTCCGTCTCCAG 462
Db 2 1leaGleuThAlaAlaAspHisArgGlnleuGlnleuSerIleSerSerCysleuGln 21
QY 463 CAGCTTCCCTGCTGTGATGTGATCAG 489
Db 22 GlnleuSerleuMetIrrIleThr 30
RESULT 17
US-10-117-937-254
; Sequence 254, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 28
; TYPE: PRT
```

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; ORGANISM: Homo sapiens
US-10-117-937-254
Alignment Scores:
Pred. No.: 1.84e-15 Length: 28
Score: 28.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.56% Indels: 0
DB: 15 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x US-10-117-937-254 (1-28)
QY 406 CGACTGACTGCTGCAGACCGCCAACTGCAGCTTCATCAGCTCCTGCTCCAGAG 465
Db 1 ArgleuThrAlaAlaAspHisArgGlnleuGlnleuSerIleSerSerCysleuGln 20
QY 466 CTTTCCTGCTGTGATGTGATCAG 489
Db 21 leuSerleuMetIrrIleThr 28
RESULT 18
US-10-117-937-255
; Sequence 255, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 255
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-255
Alignment Scores:
Pred. No.: 1.84e-15 Length: 28
Score: 28.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.56% Indels: 0
DB: 15 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x US-10-117-937-255 (1-28)
QY 448 AGCTCCTGCTTCACGACGCTTCCTGTTGATGTGATCAGCAGTGTTCGCCGTG 507
Db 1 SerSerCysleuGlnGlnleuSerleuMetIrrIleThrGlnCysPheleuProVal 20
QY 508 TTTTGCTCAGCTCCTCCTCAGGG 531
Db 21 PheleuAlaGlnProProSerGly 28
RESULT 19
US-10-296-734-1398
; Sequence 1398, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
```

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APPLICANT: Ramshaw, Ian A
TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savigne
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: AU P0761/00
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1398
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: NYSOLA segment 1
US-10-296-734-1398

Alignment Scores:
Pred. No.:      1,82e-15      Length:      30
Score:          28.00        Matches:     28
Percent Similarity: 100.00%  Conservative: 28
Best Local Similarity: 100.00% Mismatches:  0
Query Match:    15.56%      Indels:      0
DB:             12          Gaps:        0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-296-734-1398 (1-30)

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QY	Db	QY	Db
1	ATGAGGCGCCAGGCGGGGACAGAGGGGTTTCAGCGGCGATCTGATGAGCCAGGAGGC	61	CTGCGATTCTGATGCGCCAGG 84
2		62	
3	MeedlnlaagiuglyargglythrglyglyserThrglyaspalaapglyProglygly 22	63	
		64	
		65	
		66	
		67	
		68	
		69	
		70	ProglyIleProaspglyProgly 30

```

RESULT 20
US-10-296-734-1434
; Sequence 1434, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1434
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: LAGBI segment 3
US-10-296-734-1434

Alignment Scores:
Pred. No.: 1.g2e-15
Score: 28.00
Percent Similarity: 100.00%
Best local Similarity: 100.00%
Query Match: 15.56%
DB: 12
Gaps: 0

Length: 30
Matches: 28
Conservative: 0
Mismatches: 0
Indels: 0
Gaps: 0

```

QY 85 GGCATATCTGCGCCCGCCAGAGAGCGGGTGCACGGCGGCGAGAGGTCCCCGGGGCGCA 144
Db 1 G1AenhlactylglyProclglylualaglylatmrglylgylyargglyProhrglyla 20
QY 145 GGGGCAAGCAAGGGGCTTCGGGGCTCG 168

Db

21 G:\alab\arg\alaser\cylpro 28

RESULT 21
US-10-296-734-1450
Sequence 1450, Application US/10296734
Publication No. US20040054137A1
GENERAL INFORMATION:
APPLICANT: Thompson, Scott A
APPLICANT: Ramshaw, Ian A
TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: AU PQT761/00
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1450
LENGTH: 30
TYPE: prt
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: LAGB1 segment 11
US-10-296-734-1450

Alignment Scores:	
Pred. No.:	7.5e-13
Score:	25.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	13.89%
DB:	12
Gaps:	0
Length:	30
Matches:	25
Conservative:	0
Mismatches:	0
Indels:	0
Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) X US-10-296-734-1450 (1-30)

445 ATCAGCTCCTGTCTCCAGCAGCTTTCCCTGTGATGTGATCAGCAGTGCCTTTCTGCCC 504

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QY      505 GTGTTTGGCTCAG 519
        |||||
Db      21 ValpheuA1aglN 25

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RESULT 22
US-10-296-734-1430
: Sequence 1430, Application US/10296734
: Publication No. US20040054137A1
: GENERAL INFORMATION:
: APPLICANT: Thompson, Scott A
: APPLICANT: Ramshaw, Ian A
: TITLE OF INVENTION: Synthetic molecules and uses therefor
: FILE REFERENCE: Savine
: CURRENT APPLICATION NUMBER: US/10/296,734
: CURRENT FILING DATE: 2003-08-04
: PRIOR APPLICATION NUMBER: AU P07761/00
: PRIOR FILING DATE: 2000-05-26
: NUMBER OF SEQ ID NOS: 1507
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 1430
: LENGTH: 30
: TYPE: PR1
: ORGANISM: Artificial
: FEATURES:
: OTHER INFORMATION: LAGP1 segment 1
US-10-296-734-1430

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Alignment Scores:	
Pred. No.:	3,1e-10
Score:	22.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
Query Match:	12.22%
Length:	30
Matches:	22
Conservative:	0
Mismatches:	0
Indels:	0

DB: 12 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-296-734-1430 (1-30)

QY 19 GGCAAGGGGCTTCAGAGCGGCATGCTGATGGCCAGAGGCCCTGGCATTCTGATGCG 78
DB 9 GYTHRGlyGlySerThrGlyAspAlaSpGlyProGlyGlyProGlyIleProAspGly 28

QY 79 CCAGGG 84
DB 29 ProGly 30

RESULT 23

US-10-164-121A-35
; Sequence 35, Application US/10164121A
; Publication No. US20030228308A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Boon, Thierry
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Traversari, Catia
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereof
; FILE REFERENCE: IUD-5771
; CURRENT APPLICATION NUMBER: US/10/164,121A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 35
; LENGTH: 20
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-121A-35

Alignment Scores:

Pred. No.: 1.82e-08 Length: 20
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.11% Indels: 0
DB: 15 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-164-121A-35 (1-20)

QY 355 CCAGGGGCTTCAGAGGAGTTCACTGTGTCGGCAACATGACTATCCGACTGACT 414
DB 1 ProGlyValIleuLeuYsgIuPheThrValSerGlyAsnIleLeuThrIleArgLeuThr 20

RESULT 24

US-10-164-078A-34
; Sequence 34, Application US/10164078A
; Publication No. US20030228325A1
; GENERAL INFORMATION:
; APPLICANT: Bilsborough, Janine
; APPLICANT: Schultz, Erwin
; APPLICANT: Panichelli, Christophe
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B18 Molecules And Uses Thereof
; FILE REFERENCE: IUD-5756
; CURRENT APPLICATION NUMBER: US/10/164,078A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 34
; LENGTH: 20
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-078A-34

Alignment Scores:

Pred. No.: 1.82e-08 Length: 20
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Query Match: 100.00% Indels: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.11% Indels: 0
DB: 15 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-164-078A-34 (1-20)

QY 355 CCAGGGGCTTCAGAGGAGTTCACTGTGTCGGCAACATGACTATCCGACTGACT 414
DB 1 ProGlyValIleuLeuYsgIuPheThrValSerGlyAsnIleLeuThrIleArgLeuThr 20

RESULT 25

US-10-313-986-492
; Sequence 492, Application US/10313986
; Publication No. US20030236209A1
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 492
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-492

Alignment Scores:

Pred. No.: 1.82e-08 Length: 20
Score: 20.00 Matches: 20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 11.11% Indels: 0
DB: 15 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-313-986-492 (1-20)

QY 31 TCGAGGGGCGATGTGATGGCCAGAGGCCCTGGCATTCTGATGGCCAGGGGCGCAAT 90
DB 1 SerThrGlyAspAlaSpGlyProGlyGlyProGlyIleProAspGlyProGlyGlyAsn 20

RESULT 26

US-10-313-986-493
; Sequence 493, Application US/10313986
; Publication No. US20030236209A1
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 493
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-493

Alignment Scores:

Pred. No.: 1.82e-08 Length: 20
Score: 20.00 Matches: 20

Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 11.11%
DB: 15
Conservative: 0
Matches: 0
Indels: 0
Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-313-986-493 (1-20)

QY 61 CCTGCGATCTTCGATGCGCCAGGGGCGCATGTGCGCGCCGAGAGAGCGGGTCCAGC 120
DB 1 Trrllettrnglncyspneleuprovapneleualaglnproserglyglnharg 20

RESULT 27
US-10-313-986-494

Sequence 494, Application US/10313986
Publication No. US20030236209A1
GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.

APPLICANT: McNabb, Andria

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Reed, Steven G.

APPLICANT: Wang, Tonglong

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C19

CURRENT FILING DATE: 2002-12-04

CURRENT FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 560

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 494

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

US-10-313-986-494

Alignment Scores:

Pred. No.: 1.82e-08

Score: 20.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 11.11%

DB: 15

US-10-023-182-1_COPY_54_593 (1-540) x US-10-313-986-494 (1-20)

QY 271 TACTCGCGATGCTTCGCGCCAGCGCATGTGAGAGAGCGCGCCGAGAGCGCTGCGC 330
DB 1 TyrrleualawetProPhelalathrPrometGluLaGluLeuAlaArgYserLeuAla 20

RESULT 28

US-10-313-986-495

Sequence 495, Application US/10313986

Publication No. US20030236209A1

GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.

APPLICANT: McNabb, Andria

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C19

CURRENT FILING DATE: 2002-12-04

CURRENT FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 560

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 495

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

US-10-313-986-495

Alignment Scores:

Pred. No.: 1.82e-08

Length: 20

Score: 20.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 11.11%
DB: 15
Matches: 20
Conservative: 0
Matches: 0
Indels: 0
Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-313-986-495 (1-20)

QY 481 TGAATCAGCAGTCCTTTCTGCGCGCGCTGTTTGTGCTAGCCTCCCTCAGGGCAGAGCGCC 540
DB 1 Trrllettrnglncyspneleuprovapneleualaglnproserglyglnharg 20

RESULT 29

US-10-313-986-496

Sequence 496, Application US/10313986

Publication No. US20030236209A1

GENERAL INFORMATION:

APPLICANT: Foy, Teresa M.

APPLICANT: McNabb, Andria

APPLICANT: Watanabe, Yoshihiro

APPLICANT: Reed, Steven G.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C19

CURRENT FILING DATE: 2002-12-04

CURRENT FILING DATE: 2002-12-04

NUMBER OF SEQ ID NOS: 560

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 496

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

US-10-313-986-496

Alignment Scores:

Pred. No.: 1.82e-08

Score: 20.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 11.11%

DB: 15

US-10-023-182-1_COPY_54_593 (1-540) x US-10-313-986-496 (1-20)

QY 121 GCGCGCAGAGTCCCGCGCGCGCAGGGCAGAGGCGCTTGGGCGCGGAGAGCGGCC 180
DB 1 GlyglylArgglyProArgglyAlaGlyAlaAlaArgAlaSerGlyProGlyGlyAla 20

RESULT 30

US-10-364-614-5

Sequence 5, Application US/10364614

Publication No. US20030175250A1

GENERAL INFORMATION:

APPLICANT: JAGER, Elke

APPLICANT: KNUTH, Alexander

APPLICANT: OLD, Lloyd

APPLICANT: Gnajatic, Sacha

TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF

FILE REFERENCE: LUD 5726.1 CIP

CURRENT FILING DATE: 2003-02-24

CURRENT FILING DATE: 2003-02-24

PRIOR APPLICATION NUMBER: US 60/355,828

PRIOR FILING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.2

SEQ ID NO 5

LENGTH: 18

TYPE: PRT

ORGANISM: Homo sapiens

US-10-364-614-5

Alignment Scores:

Pred. No.: 1.03e-06 Length: 18
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.00% Indels: 0
DB: 14 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-364-614-5 (1-18)

QY 253 AGCCGCTCTGAGTTCCTACCTGCGCATGCTTTCGCGACACCCATGGAACA 306
DB 1 SerATgLeuAlaMeCPheAlaThrProMetGluAlaIaArgArGser 18

RESULT 31
US-10-364-614-6
; Sequence 6, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: Gnifatic, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 CIP
; CURRENT APPLICATION NUMBER: US/10/364,614
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-6

Alignment Scores:
Pred. No.: 1.03e-06 Length: 18
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.00% Indels: 0
DB: 14 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-364-614-6 (1-18)

QY 271 TACCTGCGCATGCTTTCGCGACACCCATGGAAGAGAGCGCCGCGAGAGC 324
DB 1 TylLeuAlaMeCPheAlaThrProMetGluAlaIaArgArGser 18

RESULT 32
US-10-364-614-7
; Sequence 7, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: Gnifatic, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 CIP
; CURRENT APPLICATION NUMBER: US/10/364,614
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-7

Alignment Scores:
Pred. No.: 1.03e-06 Length: 18
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.00% Indels: 0
DB: 14 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-364-614-7 (1-18)

QY 307 GAGCTGGCCGAGAGAGCGCCGAGAGAGCGCCGAGAGAGCGCTTCCGTCGAGGG 360
DB 1 GluLeuAlaArgArGserLeuAlaGlnAspAlaProPheProValProGly 18

RESULT 33
US-10-164-121A-36
; Sequence 36, Application US/10164121A
; Publication No. US20030228308A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Boon, Thierry
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Traversari, Catra
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5771
; CURRENT APPLICATION NUMBER: US/10/164,121A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 36
; LENGTH: 18
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-121A-36

Alignment Scores:
Pred. No.: 1.03e-06 Length: 18
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.00% Indels: 0
DB: 15 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-164-121A-36 (1-18)

QY 415 GCTGAGACACCGCCAGCTCTGCATGAGCTCTCTCTCCAGACAGCTT 468
DB 1 AlaAlaAspHisArgGlnLeuGlnLeuSerIleSerSerCysLeuGlnGlnLeu 18

RESULT 34
US-10-164-078A-35
; Sequence 35, Application US/10164078A
; Publication No. US20030228325A1
; GENERAL INFORMATION:
; APPLICANT: Blisborough, Janine
; APPLICANT: Schultz, Brian
; APPLICANT: Panichelli, Christophe
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B18 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5756
; CURRENT APPLICATION NUMBER: US/10/164,078A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 35
; LENGTH: 18
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-078A-35

Alignment Scores:
Pred. No.: 1.03e-06 Length: 18

Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.00% Indels: 0
DB: 15 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-164-078A-35 (1-18)

QY 415 GCTGAGACCAACCGCACTGACGCTTCATCAGCTCCTGCTTCAGAGCTT 468

Db 1 AAlaAlaAspHisArgGlnLeuGlnLeuSerHisSerCysLeuGlnGlnLeu 18

RESULT 35

US-10-296-734-1420

; Sequence 1420, Application US/10296734

; Publication No. US20040054137A1

; GENERAL INFORMATION:

; APPLICANT: Thompson, Scott A

; APPLICANT: Ramshaw, Ian A

; TITLE OF INVENTION: Synthetic molecules and uses therefor

; FILE REFERENCE: Savine

; CURRENT APPLICATION NUMBER: US/10/296,734

; PRIOR FILING DATE: 2003-08-04

; PRIOR APPLICATION NUMBER: AU PQ7761/00

; NUMBER OF SEQ ID NOS: 1507

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1420

; LENGTH: 19

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: NYSOLA segment 12

US-10-296-734-1420

Alignment Scores:

Pred. No.: 7.57e-06 Length: 19
Score: 17.00 Matches: 17
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 9.44% Indels: 0
DB: 12 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-296-734-1420 (1-19)

QY 490 CAGTGGCTTTGCGCCGCTGTTTGGCTGAGCTCCCTCAGGCGAGAGCGC 540

Db 1 GlnCysPheLeuProValPheLeuAlaGlnProProSerGlyGlnArgArg 17

RESULT 36

US-10-296-734-1428

; Sequence 1428, Application US/10296734

; Publication No. US20040054137A1

; GENERAL INFORMATION:

; APPLICANT: Thompson, Scott A

; APPLICANT: Ramshaw, Ian A

; TITLE OF INVENTION: Synthetic molecules and uses therefor

; FILE REFERENCE: Savine

; CURRENT APPLICATION NUMBER: US/10/296,734

; PRIOR FILING DATE: 2003-08-04

; PRIOR APPLICATION NUMBER: AU PQ7761/00

; NUMBER OF SEQ ID NOS: 1507

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1428

; LENGTH: 17

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: NYSOLA segment 4

US-10-296-734-1428

Alignment Scores:

Pred. No.: 0.000426 Length: 17
Score: 15.00 Matches: 15
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 8.33% Indels: 0
DB: 12 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-296-734-1428 (1-17)

QY 170 GAGAGGCGCCCCCGGGGCTCCGATGCGCGCGCGCTTCAGGCGC 214

Db 1 GlnGlnAlaProArgGlyValArgMetAlaAlaArgLeuGlnGly 15

RESULT 37

US-10-296-734-1446

; Sequence 1446, Application US/10296734

; Publication No. US20040054137A1

; GENERAL INFORMATION:

; APPLICANT: Thompson, Scott A

; APPLICANT: Ramshaw, Ian A

; TITLE OF INVENTION: Synthetic molecules and uses therefor

; FILE REFERENCE: Savine

; CURRENT APPLICATION NUMBER: US/10/296,734

; PRIOR FILING DATE: 2003-08-04

; PRIOR APPLICATION NUMBER: AU PQ7761/00

; NUMBER OF SEQ ID NOS: 1507

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1446

; LENGTH: 30

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: LAGEL segment 9

US-10-296-734-1446

Alignment Scores:

Pred. No.: 0.00291 Length: 30
Score: 14.00 Matches: 14
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.78% Indels: 0
DB: 12 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-296-734-1446 (1-30)

QY 403 ATCCGACTGACTGCTGCAACCAACCGCACTGACGCTTCC 444

Db 17 IleArgLeuThrAlaAlaAspHisArgGlnLeuGlnLeuSer 30

RESULT 38

US-10-296-734-1436

; Sequence 1436, Application US/10296734

; Publication No. US20040054137A1

; GENERAL INFORMATION:

; APPLICANT: Thompson, Scott A

; APPLICANT: Ramshaw, Ian A

; TITLE OF INVENTION: Synthetic molecules and uses therefor

; FILE REFERENCE: Savine

; CURRENT APPLICATION NUMBER: US/10/296,734

; PRIOR FILING DATE: 2003-08-04

; PRIOR APPLICATION NUMBER: AU PQ7761/00

; NUMBER OF SEQ ID NOS: 1507

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 1436

; LENGTH: 30

; TYPE: PRT

; ORGANISM: Artificial

; FEATURE:

; OTHER INFORMATION: LAGEL segment 4

US-10-296-734-1436

Alignment Scores:

```

Alignment Scores:
Pred. No.: 0 0216 Length: 30
Score: 13.00 Matches: 13
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 7.22% Indels: 0
DB: 12 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-296-734-1436 (1-30)
OY 130 GGTCCCCGGGGGCGACGAGCGGCGCTCGGGGCGG 168
|||||
Db 1 G1YProArgG1YAlaG1YAlaAlaArgAlaSerG1YPro 13
|||||

RESULT 39
US-10-296-734-1438
Sequence 1438, Application US/10296734
Publication No. US20040054137A1
GENERAL INFORMATION:
APPLICANT: Thompson, Scott A
APPLICANT: Ramshaw, Ian A
TITLE OF INVENTION: Synthetic molecules and uses therefor
FILE REFERENCE: Savine
CURRENT APPLICATION NUMBER: US/10/296,734
PRIOR FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: AU P07761/00
PRIOR FILING DATE: 2000-05-26
NUMBER OF SEQ ID NOS: 1507
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1438
LENGTH: 30
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: LAGEL segment 5
US-10-296-734-1438

Alignment Scores:
Pred. No.: 0.161 Length: 30
Score: 12.00 Matches: 12
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.67% Indels: 0
DB: 12 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-296-734-1438 (1-30)
OY 175 GGGCGCGGGGGGTGGCGATGGGGCGGCGCTTCA 210
|||||
Db 1 G1YAlaProArgG1YProHisG1YAlaAlaSer 12
|||||

RESULT 40
US-09-751-798-4
Sequence 4, Application US/09751798
Patent No. US20020010321A1
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-tseug; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

```

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1  COMPUTER:  IBM
2  OPERATING SYSTEM:  PC-DOS
3  SOFTWARE:  WordPerfect
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER:  US/09/751,798
6  FILING DATE:
7  PRIOR APPLICATION DATA:
8  APPLICATION NUMBER:  09/062,422
9  FILING DATE:
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER:  08/725,182
12 FILING DATE:  October 3, 1996
13 ATTORNEY/AGENT INFORMATION:
14 NAME:  Hanson, No. US2002010321A1man D.
15 REGISTRATION NUMBER:  30,946
16 REFERENCE/DOCKET NUMBER:  LUD 5466.3
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE:  (212) 752-5958
19 TELEFAX:  (212) 752-5958
20 INFORMATION FOR SEQ ID NO: 4:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH:  11 amino acids
23 TYPE:  amino acid
24 TOPOLOGY:  linear
25
26 US-09-751-798-4
27
28 Alignment Scores:
29 Pred. No.:
30 Score:  1.39      Length:  11
31 Percent Similarity:  11.00      Matches:  11
32 Best Local Similarity:  100.00%   Conservative:  0
33 Query Match:  6.11%      Mismatches:  0
34 DB:  9      Indels:  0
35      Gaps:  0
36
37 US-10-023-182-1_COPY_54_593 (1-540) x US-09-751-798-4 (1-11)
38
39 Qy      469  TCCCTGTTGATGCGATCAGCAGTGTCTG 501
40      |||||
41 Db      1  SerLeuLeuMetTrpIleInGInCysPheLeu 11
42
43 RESULT 41
44 US-09-766-889A-50
45 Sequence 50. Application US/09766889A
46 Patent No. US20020164654A1
47 GENERAL INFORMATION:
48 APPLICANT:  Luiten, Rosalie
49 APPLICANT:  Boon-Falleur, Thierry
50 APPLICANT:  van der Bruggen, Pierre
51 APPLICANT:  Stroobant, Vincent
52 APPLICANT:  Demotte, Nathalie
53 APPLICANT:  Schultz, Erynn
54 TITLE OF INVENTION:  MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
55 FILE REFERENCE:  L0461/77104
56 CURRENT APPLICATION NUMBER:  US/09/766,889A
57 CURRENT FILING DATE:  2001-01-19
58 PRIOR APPLICATION NUMBER:  US 60/177,242
59 PRIOR FILING DATE:  2000-01-20
60 PRIOR APPLICATION NUMBER:  US 60/243,212
61 PRIOR FILING DATE:  2000-10-25
62 NUMBER OF SEQ ID NOS: 59
63 SOFTWARE:  FastSeq for Windows Version 3.0
64 SEQ ID NO 50
65 LENGTH:  11
66 TYPE:  PRT
67 ORGANISM:  Homo sapiens
68 US-09-766-889A-50
69
70 Alignment Scores:
71 Pred. No.:
72 Score:  1.39      Length:  11
73 Percent Similarity:  11.00      Matches:  11
74 Best Local Similarity:  100.00%   Conservative:  0
75 Query Match:  6.11%      Mismatches:  0
76      Indels:  0
77      Gaps:  0

```


DB: 9 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-09-766-889A-50 (1-11)

QY 469 TCCCTGTTGATGATCAGCAGGCTTTCTG 501
Db 1 SerleuNeuMetriPleThrIncYsPheLeu 11

RESULT 42
US-10-218-095-45

Sequence 45, Application US/10218095
Publication No. US2004003541A1
GENERAL INFORMATION:
APPLICANT: Zhang, Yi
APPLICANT: Stroobant, Vincent
APPLICANT: Ruoso, Vincenzo
APPLICANT: Boon-Falleur, Thierry
APPLICANT: van der Bruggen, Pierre
TITLE OF INVENTION: MAGE-A4 ANTIGENIC PEPTIDES AND USES THEREOF
FILE REFERENCE: 100461/70137
CURRENT APPLICATION NUMBER: US/10/218,095
CURRENT FILING DATE: 2002-08-13
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.1
SEQ ID NO 45
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-10-218-095-45

Alignment Scores:
Pred. No.: 1.39 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-218-095-45 (1-11)

QY 469 TCCCTGTTGATGATCAGCAGGCTTTCTG 501
Db 1 SerleuNeuMetriPleThrIncYsPheLeu 11

RESULT 43
US-10-023-182-4

Sequence 4, Application US/10023182
Publication No. US2002016465A1
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
Chen, Yao-tseng; Scanlan, Matthew;
Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
Associated Proteins, Uses Thereof,
Truncated Forms of NY-ESO-1, and HLA
Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US2002016465A1man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-023-182-4

Alignment Scores:
Pred. No.: 1.39 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-023-182-4 (1-11)

QY 469 TCCCTGTTGATGATCAGCAGGCTTTCTG 501
Db 1 SerleuNeuMetriPleThrIncYsPheLeu 11

RESULT 44
US-10-161-097-33

Sequence 33, Application US/10161097
Publication No. US20030096404A1
GENERAL INFORMATION:
APPLICANT: ROSENZWEIG, Michael
APPLICANT: PYKETT, Mark J.
APPLICANT: SCADEN, David T.
APPLICANT: POZNANSKY, Mark C.
TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
TITLE OF INVENTION: DEVICES
FILE REFERENCE: C1005/7012/KA/ERG
CURRENT APPLICATION NUMBER: US/10/161,097
CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US/09/574,749
PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US 60/107,972
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: PCT/US99/26795
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 09/524,749
PRIOR FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Homo Sapiens source
US-10-161-097-33

Alignment Scores:
Pred. No.: 1.39 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 6.11% Indels: 0
DB: 14 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-161-097-33 (1-11)

QY 469 TCCTGTTGATGTGATCAGCAGTCTTCTG 501

DB 1 SerLeuLeuMetTrpIleThrgInCysPheLeu 11

RESULT 45

US-10-170-832-79

/ Sequence 79, Application US/10170832

/ Publication No. US20030110792A1

/ GENERAL INFORMATION:

/ APPLICANT: Chaux, Pascal

/ APPLICANT: Vantomme, Valrie

/ APPLICANT: Stroobant, Vincent

/ APPLICANT: Boon-Falleur, Thierry

/ APPLICANT: van der Bruggen, Pierre

/ APPLICANT: Thielemans, Kris

/ APPLICANT: Cortbals, Jurgen

/ TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES

/ FILE REFERENCE: L0461/7052

/ CURRENT APPLICATION NUMBER: US/10/170,832

/ CURRENT FILING DATE: 2002-06-12

/ PRIOR APPLICATION NUMBER: US/09/166,448

/ NUMBER OF SEQ ID NOS: 81

/ SOFTWARE: FaSTSeq for Windows Version 3.0

/ SEQ ID NO 79

/ LENGTH: 11

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-170-832-79

Alignment Scores:

Pred. No.: 1.39 Length: 11

Score: 11.00 Matches: 11

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 6.11% Indels: 0

DB: 14 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x US-10-170-832-79 (1-11)

QY 469 TCCTGTTGATGTGATCAGCAGTCTTCTG 501

DB 1 SerLeuLeuMetTrpIleThrgInCysPheLeu 11

Search completed: July 19, 2004, 12:18:10
Job time : 46 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 19, 2004, 12:12:40 ; Search time 26 Seconds
(without alignments)
3995.648 Million cell updates/sec

Title: US-10-023-182-1_COPY_54_593

Perfect score: 100
Sequence: 1 ATGCAGGCGCCGAGGCGCGG.....CTCCCTCAGGCGCAGAGGCGC 540

Scoring table: OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283366 seqs, 96191526 residues

Word size: 1

Total number of hits satisfying chosen parameters: 22756

Minimum DB seq length: 5

Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=x1p
-Q=/cgn2.1/USPTO_spool_p/US10023182/runat.19072004.125308.4301/app_query.fasta_1.711
-DB=FIR_78 -QFMT=fastan -SUFFIX=ol1.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=b1ts -START=1 -END=-1 -MATRIX=ol1go -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=45 -MODE=LOCAL -OUTFMT=prto
-NORM=ext -HEARSIZE=500 -MINLEN=5 -MAXLEN=50
-USER=US10023182.CCGN.1.1.38 @runat.19072004.125308.4301 -NCP=6 -ICU=3
-NO_MMAP -LARGEOUTERY -NEG_SCORES=0 -WAIT -DSFLOCK=100 -LONGLAG
-DEV_TIMEOUT=150 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database :

1: pir78:*
2: pir1:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	3.9	20	2	S19616
2	3.4	9	2	2	S26508
3	3.3	16	2	2	S54271
4	3.4	20	2	2	A39543
5	3.4	26	2	2	S78761
6	3.4	30	2	2	B39543
7	3.4	36	2	2	B95145
8	3.4	36	2	2	A82496
9	3.3	38	2	2	P10187
10	3.4	39	2	2	A46662
11	3.3	39	2	2	B81897
12	3.4	40	2	2	G82620
13	3.4	41	2	2	E24802
14	3.4	44	2	2	D35878

C 15	6	3.4	49	2	T37008	hypothetical prote
C 16	5	2.8	10	2	B38887	T-cell receptor ga
C 17	5	2.8	10	2	A59173	nuclease Bhl (BC 3
C 18	5	2.8	11	1	XAVIRH	bradykinin-potent
C 19	5	2.8	11	2	PT0214	T-cell receptor be
C 20	5	2.8	12	2	S49547	hypothetical prote
C 21	5	2.8	12	2	I39390	acetylcholine rece
C 22	5	2.8	12	2	PH0936	T-cell receptor be
C 23	5	2.8	13	2	S09716	2S albumin large c
C 24	5	2.8	13	2	PH1772	T cell receptor al
C 25	5	2.8	14	2	A61362	bradykinin-like pe
C 26	5	2.8	14	2	PH0945	T-cell receptor be
C 27	5	2.8	15	2	A47628	Fc gamma receptor
C 28	5	2.8	15	2	A42413	T-cell antigen rec
C 29	5	2.8	15	2	A42413	Ig heavy chain V r
C 30	5	2.8	16	2	C28587	T-cell receptor be
C 31	5	2.8	16	2	J70609	leukocyte chematt
C 32	5	2.8	16	2	G53284	T-cell receptor be
C 33	5	2.8	16	2	PH1580	Ig H chain V-D-J r
C 34	5	2.8	17	2	PH0587	tyrosine 3-monooxy
C 35	5	2.8	17	2	S57519	T cell receptor be
C 36	5	2.8	18	2	I52614	u-plasminogen acti
C 37	5	2.8	18	2	S54272	CtC 75 protein - h
C 38	5	2.8	19	2	G56819	PS I complex subun
C 39	5	2.8	19	2	S43624	cytochrome-c oxida
C 40	5	2.8	19	2	PH1330	Ig heavy chain DJ
C 41	5	2.8	19	2	S25715	hypothetical prote
C 42	5	2.8	20	2	S68028	iodothronine 5'-mo
C 43	5	2.8	20	2	P00544	capsid protein VP5
C 44	5	2.8	20	2	PS0028	flagellar motor sw
C 45	5	2.8	20	2	PQ0688	photosystem I 14.0

ALIGNMENTS

RESULT 1
S19616
globin - polychaete (Eudistylia vancouveri) (fragment)
N/Alternate names: chlorocrocin
C/Species: Eudistylia vancouveri
C/Date: 19-Mar-1997 #sequence_revision 10-Oct-1997 #text_change 05-Dec-1998
C/Accession: S19616
R/Qabar, A.N.; Stern, M.S.; Walz, D.A.; Chiu, J.T.; Timkovich, R.; Wall, J.S.; Kapp, O.H.
J. Mol. Biol. 222, 1109-1129, 1991
A/Title: Hierarchy of globin complexes. The quaternary structure of the extracellular ch
A/Reference number: S19532; MUID:92106333; PMID:1762147
A/Accession: S19616
A/Molecule type: protein
A/Residues: 1-20 <QAB>
C/Complex: dodecamers, each consisting of a trimer of tetramers of globin chains; dodecan
C/Keywords: calcium; dodecamer; heme; homotrimer; oxygen carrier

Alignment Scores:
Pred. No.: 450
Score: 7.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 3.89%
DB: 2
Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x S19616 (1-20)

QY 112 GGTGCGAGGCGCGCAGAGGT 132
Db 1 GlyAlaThrGlyGlyArgGly 7

RESULT 2
S26508
collagen alpha 2(VI) chain - bovine (fragment)
C/Species: Bos primigenius taurus (cattle)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Dec-1998
C/Accession: S26508
R/Jander, R.; Rautenberg, J.; Gianville, R.W.

Err. J. Biochem. 133, 39-46, 1983
A>Title: Further characterization of the three polypeptide chains of bovine and human sh
A:Reference number: S26506; MUID:83209648; PMID:6852033
A:Accession: S26508
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-9 <JAN>
C:Keywords: hydroxyproline
F:7/Modified site: hydroxyproline (Pro) #status experimental

Alignment Scores:
Pred. No.: 2.14e+07 Length: 9
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x S26508 (1-9)

OY 65 CCAGGCGCTCTGGCCA 48
|||||
Db 4 ProGlyProProGlyPro 9

RESULT 3
S54271
GATA-2 protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C>Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
C:Accession: S54271
R:Breuer, A.C.; Gullile, M.J.; Fear, D.J.; Partington, G.A.; Patient, R.K.
EMBO J. 14, 757-766, 1995
A>Title: Nuclear translocation of a maternal CCAT factor at the start of gastrulation
A:Reference number: S54270; MUID:95188880; PMID:7882979
A:Accession: S54271
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-16 <BRE>

Alignment Scores:
Pred. No.: 4.45e+03 Length: 16
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x S54271 (1-16)

OY 452 CCTGTCTCCAGCAGCTTT 469
|||||
Db 6 ProValSerSerSerPhe 11

RESULT 4
A39543
collagen alpha 1(IX) chain - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 15-Sep-2003
C:Accession: A39543
R:Wu, J.J.; Lark, M.W.; Chun, L.E.; Eyre, D.R.
J. Biol. Chem. 266, 5625-5628, 1991
A>Title: Sites of stromelysin cleavage in collagen types II, IX, X, and XI of cartilage.
A:Reference number: A39543; MUID:91170231; PMID:2005102
A:Accession: A39543
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <WDA>
C:Keywords: coiled coil; extracellular matrix; glycoprotein; trimer

Alignment Scores:
Pred. No.: 4.32e+03 Length: 20
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x A39543 (1-20)

OY 65 CCAGGCGCTCTGGGCCA 48
|||||
Db 15 ProGlyProProGlyPro 20

RESULT 5
S78761
ribosomal protein MRP-L18, mitochondrial - bovine (fragments)
C:Species: Bos primigenius taurus (cattle)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: S78761
R:Graack, H.R.
submitted to the Protein Sequence Database, July 1999
A:Reference number: S78760
A:Accession: S78761
A:Molecule type: protein
A:Residues: 1-16;17-26 <GRA>
C:Keywords: mitochondrion
F:1-26/Product: ribosomal protein MRP-L18 (fragment) #status experimental <MAT>

Alignment Scores:
Pred. No.: 4.17e+03 Length: 26
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x S78761 (1-26)

OY 373 CTTGAGAGCACCCTG 356
|||||
Db 21 ProSerGluAlaProLeu 26

RESULT 6
B39543
collagen alpha 2(IX) chain - bovine (fragment)
C:Species: Bos primigenius taurus (cattle)
C>Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 15-Sep-2003
C:Accession: B39543
R:Wu, J.J.; Lark, M.W.; Chun, L.E.; Eyre, D.R.
J. Biol. Chem. 266, 5625-5628, 1991
A>Title: Sites of stromelysin cleavage in collagen types II, IX, X, and XI of cartilage.
A:Reference number: A39543; MUID:91170231; PMID:2005102
A:Accession: B39543
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-26 <WDA>

Alignment Scores:
Pred. No.: 4.17e+03 Length: 26
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x B39543 (1-26)

OY 65 CCAGGCGCTCTGGGCCA 48
|||||
Db 15 ProGlyProProGlyPro 20

RESULT 7
B95145
hypothetical protein SP1253 [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C/Accession: E95145
R/Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A./Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.
A/Reference number: A95000; MUID:21357209; PMID:11463916
A/Accession: E95145
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-30 <KUR>
A/Cross-references: GB:AE005672; PIDN:AAK75358.1; PID:G14972736; GSPDB:GN00164; TIGR:SP4
C/Experimental source: strain TIGR4
C/Genetics:
A/Gene: SP1253

Alignment Scores:
Pred. No.: 4.09e+03 Length: 30
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x E95145 (1-30)

OY 314 GCCAGCTCTGCTTCATG 297
DB 14 AAlaserSerAlaserMet 19

RESULT 8
A82496
hypochemical protein VCA0143 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
C/Species: *Vibrio cholerae*
C/Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C/Accession: A82496
R/Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
charlson, D.; Ermolaeva, M.D.; Vamtheman, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A/Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
A/Reference number: A82035; MUID:20406833; PMID:10952301
A/Accession: A82496
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-36 <HEI>
A/Cross-references: GB:AE004355; GB:AE003853; MID:99657524; PIDN:AAF96056.1; GSPDB:GN001
A/Experimental source: serogroup O1; strain N16961; biotype El Tor
C/Genetics:
A/Gene: VCA0143
A/Map position: 2

Alignment Scores:
Pred. No.: 3.99e+03 Length: 36
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x A82496 (1-36)

OY 517 GAGCCAAAACACGGGCA 500
DB 8 GIProPolyThrArgAla 13

RESULT 9
PL0187
Ig lambda chain - tiger shark (tentative sequence) (fragment)
C/Species: *Galusdo caviert* (tiger shark)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 31-Mar-2000
C/Accession: PL0187

R/Schluter, S.F.; Beischel, C.J.; Martin, S.A.; Marchalonis, J.J.
Mol. Immunol. 27, 17-23, 1990
A/Title: Sequence analysis of homogeneous peptides of shark immunoglobulin light chains t
eptides of sharks and mammals.
A/Reference number: PL0186; MUID:90190677; PMID:2107332
A/Accession: PL0187
A/Molecule type: protein
A/Residues: 1-38 <SCH>
A/Experimental source: serum
C/Keywords: heterotetramer; immunoglobulin

Alignment Scores:
Pred. No.: 3.96e+03 Length: 38
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x PL0187 (1-38)

OY 58 GGCCTGCGCATTCCTGAT 75
DB 1 GIProGlyProGlyProasp 6

RESULT 10
A46662
collagen alpha 2(V) chain - bovine (fragment)
C/Species: *Bos primigenius taurus* (cattle)
C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Jul-1995
C/Accession: A46662
R/Mayne, R.; Brewton, R.G.; Mayne, P.M.; Baker, J.R.
J. Biol. Chem. 268, 9381-9386, 1993
A/Title: Isolation and characterization of the chains of type V/type XI collagen present
A/Reference number: A46662; MUID:93252802; PMID:8486632
A/Accession: A46662
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-39 <MAY>
A/Experimental source: vitreous humor
A/Note: Sequence extracted from NCBI backbone (NCBIP:131547)
C/Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology;

Alignment Scores:
Pred. No.: 3.95e+03 Length: 39
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x A46662 (1-39)

OY 65 CCAGGGCTCTCTGGGCA 48
DB 15 ProGlyProProGlyPro 20

RESULT 11
B81897
hypochemical protein NMA1288 [imported] - *Neisseria meningitidis* (strain 22491 serogroup
C/Species: *Neisseria meningitidis*
C/Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
C/Accession: B81897
R/Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A/Title: Complete DNA sequence of a serogroup A strain of *Neisseria meningitidis* 22491.
A/Reference number: A81775; MUID:20222556; PMID:10761919
A/Accession: B81897
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-39 <PAR>
A/Cross-references: GB:AL162755; GB:AL157959; MID:97379742; PIDN:CAB84540.1; PID:97379964

A:Experimental source: serogroup A, strain Z2491
A:Gene: NMA1288

Alignment Scores:

Pred. No.:	3.95e+03	Length:	39
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.33%	Indels:	0
DB:	2	Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) x B81897 (1-39)

QY 450 CTCCTGTCCTCCAGCAGCT 467

DB 7 LeuleuserProAlaAla 12

RESULT 12

G82620 hypothetical protein XP192 (imported) - Xylella fastidiosa (strain 95c)

C:Species: Xylella fastidiosa

C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000

C:Accession: G82620

C:Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A:Reference number: A82515; MUID:20365717; PMID:10910347

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: G82620

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-40 <SIM>

A:Cross-references: GB:AE004012; GB:AE003849; NID:g9107020; PIDN:AAF4728.1; GSPDB:GN001

A:Experimental source: strain 95c

R:Simpon, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre, H

as-Neto, E.; Docena, C.; El-Porty, H.; Facincani, A.P.; Ferreira, A.J.S.

submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Froh

J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kurame, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Martino, C.L.; Marques, M.V.; Martins, E

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmiter, D.A

Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva

M.; Tuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Cross-references: annotation

A:Gene: XF1922

C:Gene: XF1922

Alignment Scores:

Pred. No.:	3.94e+03	Length:	40
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.37%	Indels:	0
DB:	2	Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) x G82620 (1-40)

QY 135 GGACCTTGCCGCCGCT 118

DB 27 GlyThrSerAlaAlaArg 32

RESULT 13

E24802 cuticle protein 32 - migratory locust (fragment)

C:Species: Locusta migratoria (migratory locust)

C>Date: 22-Jul-1987 #sequence_revision 22-Jul-1987 #text_change 18-Jun-1993

C:Accession: E24802

A:Experimental source: serain A3(2)

Eur. J. Biochem. 154, 153-159, 1986

A:Reference number: A91157; MUID:86108304; PMID:3943519

A:Accession: E24802

A:Molecule type: protein

A:Residues: 1-41 <HOU>

Pred. No.:	3.92e+03	Length:	41
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.37%	Indels:	0
DB:	2	Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) x E24802 (1-41)

QY 158 GCCCTGCTGCCCTGCG 141

DB 15 AlaLeuAlaAlaProAla 20

RESULT 14

D35878 class I major histocompatibility antigen BALB-1 - mouse

C:Species: Mus musculus (house mouse)

C>Date: 12-Oct-1990 #sequence_revision 12-Oct-1990 #text_change 23-Jul-1999

C:Accession: D35878

C:Title: Recognition of the product of a novel MHC TL region gene (27(b)) by a mouse gam

A:Reference number: A35878; MUID:90335964; PMID:2379238

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-44 <ITO>

A:Cross-references: GB:M3247; NID:g199665; PIDN:AAA39696.1; PID:g199666

A:Superfamily: class I histocompatibility antigen; immunoglobulin homology

Alignment Scores:

Pred. No.:	3.89e+03	Length:	44
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	3.37%	Indels:	0
DB:	2	Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) x D35878 (1-44)

QY 28 CCCCTGTCGCCGCCCTT 11

DB 32 ProLeuCySProGlyLeu 37

RESULT 15

T37008 hypothetical protein SCJ11.37 - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C>Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T37008

R:Oliver, K.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, August 1999

A:Reference number: Z21618

A:Accession: T37008

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Gene: SCJ11.37

A:Accession: T37008

A:Molecule type: DNA

A:Residues: 1-49 <OLI>

A:Cross-references: EMBL:AL109949; PIDN:CA852922.1; GSPDB:GN00070; SCOEDB:SCJ11.37

A:Experimental source: serain A3(2)

A:Gene: SCOEDB:SCJ11.37

C:Gene: SCOEDB:SCJ11.37

Alignment Scores:

Pred. No.:	3.83e+03	Length:	49
Score:	6.00	Matches:	6
Percent Similarity:	100.00%	Conservative:	0

Score: 6.00

Percent Similarity: 100.00%

Conservative: 0

Matches: 6

Indels: 0

Gaps: 0

DB: 2

Indels: 0

Mismatches: 0

Conservative: 0

Matches: 6

Length: 49

Score: 6.00

Percent Similarity: 100.00%

Conservative: 0

Matches: 6

Indels: 0

Gaps: 0

DB: 2

Indels: 0

Mismatches: 0

Conservative: 0

Matches: 6

Length: 49

Score: 6.00

Percent Similarity: 100.00%

Conservative: 0

Matches: 6

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x T37008 (1-49)

QY 498 AAAGCAGTCGATGATCA 481
DB 39 LysAlaLeuArgAspPro 44

RESULT 16
B38887
T-cell receptor gamma chain (5c.3) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: B38887
R:Whiteall, M.; Mosley, R.L.; Whetzel, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.
Mol. Cell. Biol. 11, 5902-5909, 1991
A:Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene
A:Reference number: A11946; MUID:92049316; PMID:1658619
A:Accession: B38887
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-10 <WHE>
C:Keywords: T-cell receptor

Alignment Scores:
Pred. No.: 4.54e+04 Length: 10
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x B38887 (1-10)

QY 338 GCATCTGCGCCAGG 324
DB 1 AlaSerTrpAlaArg 5

RESULT 17
A59173
nuclease Bnl (EC 3.1.-.-) - Basidiobolus hapcosporus (fragment)
C:Species: Basidiobolus hapcosporus
C:Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000
C:Accession: A59173
R:Desai, N.; Shankar, V.
submitted to the Protein Sequence Database, February 2000
A:Description: Single-strand-specific, guanylic acid preferential nuclease from Basidiobolus
A:Reference number: A59173
A:Accession: A59173
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <DEB>
A:Note: extracellular, single-strand-specific nuclease
C:Keywords: hydrolase

Alignment Scores:
Pred. No.: 4.54e+04 Length: 10
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x A59173 (1-10)

QY 61 GGCCCTCTGGGCAT 47
DB 2 GlyLeuLeuGlyHis 6

RESULT 18
XAVIBH

bradykinin-potentiating peptide - hals viper
N:Alternate names: BPP
C:Species: Agkistrodon halys (hals viper)
C:Date: 30-Sep-1988 #sequence_revision 30-Sep-1988 #text_change 05-Aug-1994
C:Accession: J00002
R:Chi, C.W.; Wang, S.Z.; Xu, L.G.; Wang, M.Y.; Lo, S.S.; Huang, W.D.
Peptides 6, 339-342, 1985
A:Title: Structure-function studies on the bradykinin potentiating peptide from Chinese viper
A:Reference number: J00002; MUID:86177022; PMID:3008123
A:Accession: J00002
A:Molecule type: protein
A:Residues: 1-11 <CHI>
C:Comment: Because this peptide both inhibits the activity of the angiotensin-converting enzyme
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor; antihypertensive; bradykinin; pyrogl
F1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

Alignment Scores:
Pred. No.: 4.48e+04 Length: 11
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x XAVIBH (1-11)

QY 249 CGGCCCTGCGCCG 235
DB 3 ArgProProGlyPro 7

RESULT 19
PT0214
T-cell receptor beta chain V-J region (4-1-L.6) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997
C:Accession: PT0214
R:Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.
J. Exp. Med. 173, 1091-1097, 1991
A:Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted
A:Reference number: PT0209; MUID:91217621; PMID:1902501
A:Accession: PT0214
A:Molecule type: mRNA
A:Residues: 1-11 <NAK>
C:Keywords: T-cell receptor

Alignment Scores:
Pred. No.: 4.48e+04 Length: 11
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.78% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x PT0214 (1-11)

QY 232 TCGCGGCCAGCGG 246
DB 1 CysGlyAlaArgGly 5

RESULT 20
S49547
hypothetical protein 2 (insertion sequence IS1110) - Mycobacterium avium
C:Species: Mycobacterium avium
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 07-May-1999
C:Accession: S49547
R:Perez, M.H.; Fomukong, N.G.; Hellyer, T.; Brown, I.N.; Dale, J.W.
Mol. Microbiol. 12, 717-724, 1994
A:Title: Characterization of IS1110, a highly mobile genetic element from Mycobacterium
A:Reference number: S49546; MUID:94328924; PMID:8052124
A:Accession: S49547
A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-12 <PER>
A:Cross-references: EMBL:Z23003

Alignment Scores:

Pred. No.: 4.43e+04 Length: 12
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x S49547 (1-12)

QY 266 TCAGAGCGCGCTC 252

DB 4 SerSerArgArgLeu 8

RESULT 21

I39390
acetylcholine receptor (alternative exon 5b) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 21-Jul-2000
C:Accession: I39390
R:Milnovilovic, M.; Mai, Y.; Herbstreith, M.; Rubboli, F.; Tarroni, P.; Clementi, F.; Ros
Biochem. Biophys. Res. Commun. 197, 137-144, 1993
A:Title: Splicing of an anti-sense Alu sequence generates a coding sequence variant for
A:Reference number: I39390; MUID:94071933; PMID:8250918
A:Accession: I39390
A:Status: preliminary; translation not shown
A:Molecule type: mRNA
A:Residues: 1-12 <RES>
A:Cross-references: GB:L18973; NID:9441143; PID:AAA6792.1; PID:9441144
C:Keywords: alternative splicing; neurotransmitter receptor

Alignment Scores:

Pred. No.: 4.43e+04 Length: 12
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x I39390 (1-12)

QY 446 ATGAGAGCTGCAGT 432

DB 1 MetGluSerCysSer 5

RESULT 22

PH0936
T-cell receptor beta chain V-D-J region (clone 7) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0936
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0936
A:Molecule type: mRNA
A:Residues: 1-12 <GOL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
C:Keywords: T-cell receptor

Alignment Scores:

Pred. No.: 4.43e+04 Length: 12
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.78% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x PH0936 (1-12)

QY 366 TCTGAGAGCTTCAC 380

DB 4 SerGluGlyValHis 8

RESULT 23

S09716
2S albumin large chain (1 and 2) nII - rape (fragments)
N:Alternate names: 2S albumin large chain nII
C:Species: Brassica napus (rape)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 21-Aug-1998
R:Monasive, R.I.; Mendez-Artae, L.; Lopez-Otin, C.; Rodriguez, R.
FEBS Lett. 263, 209-212, 1990
A:Title: beta-Turns as structural motifs for the proteolytic processing of seed proteins.
A:Reference number: S09720; MUID:90242974; PMID:2185951
A:Accession: S09716

A:Molecule type: protein
A:Residues: 1-9/10-13 <MON>
A:Experimental source: seed
A:Note: 3-Ser was also found
A:Accession: S09718
A:Molecule type: protein
A:Residues: 1-9/10-13 <MO2>
A:Experimental source: seed
A:Accession: S09717
A:Molecule type: protein
A:Residues: 1-9/10-13 <MO3>
A:Experimental source: seed

Alignment Scores:

Pred. No.: 4.39e+04 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x S09716 (1-13)

QY 176 CCTGCTCCGGGCGCC 162

DB 8 ProAlaGlyGlnLeu 12

RESULT 24

PH1772
T cell receptor alpha chain V region (clone 2V alpha 23-3) - human (fragment)
C:Species: Homo sapiens (man)
C>Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C:Accession: PH1772
R:Porcellini, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A:Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood (C)
A:Reference number: PH1754; MUID:93301585; PMID:8391057
A:Accession: PH1772
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-13 <POR>

Alignment Scores:

Pred. No.: 4.39e+04 Length: 13
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x PH1772 (1-13)

QY 321 CCTGCGGCGAGCTC 307

DB 6 ProAlaGlyGlnLeu 10


```
RESULT 25
A61362
bradykinin-like peptide III - Japanese pond frog
C:Species: Rana nigromaculata (Japanese pond frog)
C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 02-Sep-2000
C:Accession: A61362
R:Nakajima, T.
Chem. Pharm. Bull. 16, 2088-2089, 1968
A:Title: On the third active peptide on smooth muscle in the skin of Rana nigromaculata
A:Reference number: A61362; MUID:69117202; PMID:5751736
A:Accession: A61362
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-14 <NAK>
C:Superfamily: unassigned animal peptides
C:Keywords: skin

Alignment Scores:
Pred. No.: 4.34e+04 Length: 14
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
Gaps: 0
DB: 2

US-10-023-182-1_COPY_54_593 (1-540) x A61362 (1-14)

QY 119 GTGGCAGCCGCTCT 105
DB 10 VALAIAProAlaSer 14

RESULT 26
PH0945
T-cell receptor beta chain V-D-J region (clone 16) - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C:Accession: PH0945
R:Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A:Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
A:Reference number: PH0891; MUID:92078857; PMID:1836012
A:Accession: PH0945
A:Molecule type: mRNA
A:Residues: 1-14 <GOL>
A:Experimental source: complete Freund's adjuvant-immunized lymph node
A:Note: the authors translated the codon TTC for residue 11 as Ser
C:Keywords: T-cell receptor

Alignment Scores:
Pred. No.: 4.34e+04 Length: 14
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
Gaps: 0
DB: 2

US-10-023-182-1_COPY_54_593 (1-540) x PH0945 (1-14)

QY 266 TCAAGCAGCGCGCTC 252
DB 3 SerSerArgArgLeu 7

RESULT 27
A47628
Fc gamma receptor II (CD32) - human (fragments)
C:Species: Homo sapiens (man)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: A47628
R:Wamerdam, P.A.M.; van de Winkel, J.G.J.; Goseelin, E.J.; Capel, P.J.A.
J. Exp. Med. 172, 19-25, 1990
A:Title: Molecular basis for a polymorphism of human Fc gamma receptor II (CD32).
A:Reference number: A47628; MUID:90293679; PMID:2141627
```

```
A:Accession: A47628
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-15 <WAR>
C:Keywords: Immunoglobulin receptor

Alignment Scores:
Pred. No.: 4.3e+04 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
Gaps: 0
DB: 2

US-10-023-182-1_COPY_54_593 (1-540) x A47628 (1-15)

QY 206 GCCGCGCCGCTATGC 192
DB 3 AlaAlaProProCys 7

RESULT 28
S47367
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
C:Accession: S47367
R:Lehner, P.J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T ce
A:Reference number: S47355
A:Accession: S47367
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15 <LEH>
A:Cross-references: EMBL:Z35692; NID:9527475; PIDN:CA084761.1; PID:9527476
C:Keywords: T-cell receptor

Alignment Scores:
Pred. No.: 4.3e+04 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.78% Indels: 0
Gaps: 0
DB: 2

US-10-023-182-1_COPY_54_593 (1-540) x S47367 (1-15)

QY 109 GCGGCTGCGCAGCGC 123
DB 4 AlaGlyAlaThrGly 8

RESULT 29
A42413
Ig heavy chain V region (LbL-copurifying) - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 07-May-1999
C:Accession: A42413
R:Bao, Z.; Muschler, J.; Horwitz, A.F.
J. Biol. Chem. 267, 4974-4980, 1992
A:Title: LbL, a novel, developmentally regulated, laminin-binding lectin.
A:Reference number: A42413; MUID:92165867; PMID:1531660
A:Accession: A42413
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <BAO>
C:Keywords: heterotetramer; immunoglobulin

Alignment Scores:
Pred. No.: 4.3e+04 Length: 15
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
Gaps: 0
```

DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x A42413 (1-15)

QY 430 GCGCGTGTCTTCAG 416

Db 8 GlyGlyGlyLeuGln 12

RESULT 30

C28587 T-cell receptor beta-2 chain J-B2.4 segment - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999

C/Accession: C28587

R/Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T. W.

Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985

A/Title: Organization and sequences of the diversity joining, and constant region genes

A/Reference number: A94081; MUID:86094276; PMID:3866244

A/Accession: C28587

A/Molecule type: DNA

A/Residues: 1-16 <TOY>

A/Cross-references: GB:M14159; NID:9338852; PIDN:AAA60678.1; PID:9553689

C/Keywords: T-cell receptor

QY 117 GGCACCGCCTCTCC 103

Db 10 GlyTnArgLeuSer 14

RESULT 31

JT0609 leukocyte chemoattractant peptide 6 - sheep

C/Species: Ovis orientalis aries; Ovis ammon aries (domestic sheep)

C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 19-Jan-2001

C/Accession: JT0609

R/Murdoch, W.J.; McCormick, R.J.

Biochem. Biophys. Res. Commun. 184, 848-852, 1992

A/Title: Sequence analysis of leukocyte chemoattractant peptides secreted by periovulato

A/Reference number: JT0609; MUID:92246975; PMID:1575752

A/Accession: JT0609

A/Molecule type: protein

A/Residues: 1-16 <MUR>

C/Keywords: hydroxyproline

F,3,6,9,12,15/Modified site: hydroxyproline (Pro) #stratus experimental

QY 65 CCAGGCGCTCTGGG 51

Db 3 ProGlyProProGly 7

RESULT 32

G53284 T-cell receptor beta 2 chain J region, Jbeta2.4 - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C/Accession: G53284

R/Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A/Title: Evolutionarily conserved organization and sequences of germline diversity and j/c

A/Reference number: A53284; MUID:91342695; PMID:1678859

A/Accession: G53284

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-16 <HAR>

A/Cross-references: GB:S60737; NID:9233916; PIDN:AAH19523.1; PID:9233923

A/Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBI:60745)

C/Keywords: T-cell receptor

QY 117 GGCACCGCCTCTCC 103

Db 10 GlyThrArgLeuSer 14

RESULT 33

PH1580 Ig H chain V-D-J region (wild-type clone 3) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C/Accession: PH1580

R/Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A/Reference number: PH1580; MUID:93301609; PMID:8315387

A/Accession: PH1580

A/Molecule type: DNA

A/Residues: 1-16 <LEV>

A/Experimental source: bone marrow pre-B lymphocyte

C/Keywords: immunoglobulin

QY 145 GGGCAGCAGAGGCC 159

Db 5 GlyAlaAlaArgAla 9

RESULT 34

PN0587 tyrosine 3-monooxygenase (EC 1.14.16.2) type 3 and 4 - Japanese macaque (fragment)

N/Alternate names: oxygen oxidoreductase; tetrahydropteridine; tyrosine hydroxylase

C/Species: Macaca fuscata (Japanese macaque)

C/Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 31-Mar-2000

C/Accession: PN0587

R/Richinose, H.; Ohye, T.; Fujita, K.; Yoshida, M.; Ueda, S.; Nagatsu, T.

Biochem. Biophys. Res. Commun. 195, 158-165, 1993

A/Title: Increased heterogeneity of tyrosine hydroxylase in humans.

A/Reference number: PN0575; MUID:93371398; PMID:7689834

A/Accession: PN0587

A/Molecule type: genomic RNA

A/Residues: 1-17 <RCH>

A/Cross-references: GB:J14801

A/Experimental source: Kidney

C:Comment: This enzyme catalyzes the first and rate-limiting step of catecholamine biosy
C:Superfamily: phenylalanine 4-monooxygenase
C:Keywords: bipterin; monooxygenase; oxidoreductase

Alignment Scores:

Pred. No.:	4.23e+04	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.81%	Indels:	0
DB:	2	Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) x PN0587 (1-17)

QY 243 CCGGCCCCGCATCT 229

Db 3 Progliprolaser 7

RESULT 35

S57519 T cell receptor beta chain V region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999

C:Accession: S57519 R.Burrows, S.R.; Sillins, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argact, V.P.

A:Description: T cell receptor repertoire for a viral epitope in humans is diversified b

A:Reference number: S57494

A:Accession: S57519

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-17 <BUR>

A:Cross-references: EMBL:Z49930; NID:g887494; PIDN:CAA90176.1; PID:g887495

C:Keywords: T-cell receptor

Alignment Scores:

Pred. No.:	4.23e+04	Length:	17
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.78%	Indels:	0
DB:	2	Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) x S57519 (1-17)

QY 439 CTCGCCATCAGCTCC 453

Db 7 Leuserlieser 11

RESULT 36

S52614 u-plasminogen activator receptor precursor - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000

C:Accession: S52614

R:Scoravja, E.; Grebe, A.; De Luca, P.; Helin, K.; Suh, T.T.; Degen, J.L.; Blasi, F.

A:Title: A conserved TATA-less proximal promoter drives basal transcription from the urc

A:Reference number: S52614; MUID:95329719; PMID:7605992

A:Accession: S52614

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-18 <RES>

A:Cross-references: GB:S78532; NID:g999307; PIDN:AA014289.1; PID:g4261989

C:Gene: uPAR

C:Superfamily: urokinase-type plasminogen activator receptor; Ly-6 homology

Alignment Scores:

Pred. No.:	4.2e+04	Length:	18
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0

Query Match: 2.81%

DB: 2 Indels: 0

US-10-023-182-1_COPY_54_593 (1-540) x I52614 (1-18)

QY 115 CACCCGCTCTCTG 101

Db 3 HisProleulan 7

RESULT 37

S54272 CTC 75 protein - human

C:Species: Homo sapiens (man)

C:Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 17-Mar-1999

C:Accession: S54272

R:Generach, E.; Ekerskorn, C.; Lottspeich, F.; Herzog, C.; Kuehn, K.; Poeschl, E.

EMBO J. 14, 791-800, 1995

A:Title: Purification of the sequence-specific transcription factor CTCBF, involved in ct

A:Reference number: S54272; MUID:95188883; PMID:7882982

A:Accession: S54272

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-18 <GEN>

Alignment Scores:

Pred. No.:	4.2e+04	Length:	18
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.81%	Indels:	0
DB:	2	Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) x S54272 (1-18)

QY 481 ACATCAACGGGAAA 467

Db 5 Threerthglylys 9

RESULT 38

G56819 PS I complex subunit 6 - cucumber (fragment)

C:Species: Cucumis sativus (cucumber)

C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996

C:Accession: G56819

R:Wassaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.

Biochim. Biophys. Acta 1059, 141-148, 1991

A:Title: Characterization of genes that encode subunits of cucumber PS I complex by N-ter

A:Reference number: A56819; MUID:91355209; PMID:1883835

A:Accession: G56819

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <IMA>

A>Note: sequence extracted from NCBI backbone (NCBIP:58604)

Alignment Scores:

Pred. No.:	4.17e+04	Length:	19
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.81%	Indels:	0
DB:	2	Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) x G56819 (1-19)

QY 209 GAAGCCGCGCCCA 195

Db 3 Glutalalapropro 7

RESULT 39

S43624 cytochrome-c oxidase (EC 1.9.3.1) chain IV, cardiac - rainbow trout (fragment)

C:Species: Oncorhynchus mykiss (rainbow trout)

C:Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999

C:Accession: S43624
R:Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A:Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cytochrome
A:Reference number: S43624; MUID:94237150; PMID:8181469
A:Accession: S43624
A:Molecule type: protein
A:Residues: 1-19 <PRE>
A>Note: the source is designated as *Salmo gairdneri*
A:Genetics:
A:Genome: nuclear
C:Keywords: cardiac muscle; heart; membrane-associated complex; mitochondrion; oxidoreductase

Alignment Scores:
Pred. No.: 4.17e+04 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x S43624 (1-19)

QY 282 CATGGCGAGCTAGCA 268
DB 3 HAsGlyGluValGlu 7

RESULT 40
PH1330
Ig heavy chain DJ region (clone C422-111) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PH1330
R:Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A:Title: Predominance of fetal type DJH joining in young children with B precursor lymphoma
A:Reference number: PH1302; MUID:93094761; PMID:1460419
A:Accession: PH1330
A:Molecule type: DNA
A:Residues: 1-19 <MAS>
C:Keywords: heterodimer; immunoglobulin

Alignment Scores:
Pred. No.: 4.17e+04 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x PH1330 (1-19)

QY 124 CGCCCGTGGCACCG 110
DB 15 AtgProlTPH1sPro 19

RESULT 41
S25715
Hypothetical protein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999
C:Accession: S25715; S21390
R:Bowtell, D.; Fu, P.; Simon, M.; Senior, P.
Proc. Natl. Acad. Sci. U.S.A. 89, 6511-6515, 1992
A:Title: Identification of murine homologues of the *Drosophila* Son of sevenless gene: p0
A:Reference number: S25714; MUID:9235328; PMID:1631150
A:Accession: S25715
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-19 <BOW>
A:Cross-references: EMBL:Z11578; NID:954132; PIDN:CA77665.1; PID:954133
R:Bowtell, D.D.; Fu, P.; Simon, M.A.; Senior, P.V.
submitted to the EMBL Data Library, January 1992

A:Description: Identification of murine homologues of the *Drosophila* Son of sevenless gene
A:Reference number: S21390
A:Accession: S21390
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-19 <BO2>
A:Cross-references: EMBL:Z11578; NID:954132; PIDN:CA77665.1; PID:954133

Alignment Scores:
Pred. No.: 4.17e+04 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.78% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x S25715 (1-19)

QY 174 AGCGCGCCCGCGCGG 188
DB 7 ArgArgProAlaGly 11

RESULT 42
S68028
Iodothyronine 5'-monodeiodinase - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C:Accession: S68028
R:Zhou, L.X.; Dehal, S.S.; Kupfer, D.; Morrell, S.; McKenzie, B.A.; Eccleston Jr., E.D.; Arch. Biochem. Biophys. 322, 390-394, 1995
A:Title: Cytochrome P450 catalyzed covalent binding of methoxychlor to rat hepatic, microsome
A:Reference number: S68028; MUID:96032659; PMID:7574712
A:Accession: S68028
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <ZHO>
C:Superfamily: protein disulfide-isomerase; thioredoxin homology

Alignment Scores:
Pred. No.: 4.14e+04 Length: 20
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x S68028 (1-20)

QY 161 GAGGCGCTTGCTGCC 147
DB 11 GluAlaLeuAlaAla 15

RESULT 43
P00544
capsid protein VP5 - human herpesvirus 1 (fragments)
C:Species: human herpesvirus 1
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
C:Accession: P00544
R:Davidson, M.D.; Rixon, F.J.; Davidson, A.J.
J. Gen. Virol. 73, 2709-2713, 1992
A:Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes virus
A:Reference number: P00544; MUID:93019027; PMID:1328483
A:Accession: P00544
A:Molecule type: protein
A:Residues: 1-20 <DAV>
A:Experimental source: strain 17
A:Genetics:
A:Gene: UL19
C:Keywords: capsid protein

Alignment Scores:
Pred. No.: 4.14e+04 Length: 20

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 2 Gaps: 0

Job time : 28 secs

US-10-023-182-1_COPY_54_593 (1-540) x PQ0544 (1-20)

OY 155 CTTGTCGCCCTGCG 141
DB 9 LeuAlaAlaProAla 13

RESULT 44

PS0028
flagellar motor switch protein flbd - Escherichia coli (fragment)
C:Species: Escherichia coli
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 18-Jun-1993
C:Accession: PS0028
R:Malakooti, J.; Kameda, Y.; Matsumura, P.
J. Bacteriol. 171, 2728-2734, 1989
A:Title: DNA sequence analysis, gene product identification, and localization of flagellin
A:Reference number: PS0027; MUID:89213963; PMID:2651416
A:Accession: PS0028
A:Molecule type: DNA
A:Residues: 1-20 <MAL>
C:Genetics:
A:Gene: flbd

Alignment Scores:

Pred. No.:	4.14e+04	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.78%	Indels:	0
DB:	2	Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) x PS0028 (1-20)

OY 446 TCAGTCTGCTGCC 460
DB 10 SerAlaProValSer 14

RESULT 45

PQ0688
photosystem I 14.0K B4 chain - common tobacco (fragment)
C:Species: Nicotiana tabacum (common tobacco)
C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C:Accession: PQ0688
R:Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.
Plant Physiol. 102, 1259-1267, 1993
A:Title: Molecular heterogeneity of photosystem I. psad, psaf, psah and psal are a
A:Reference number: PQ0687; MUID:94105345; PMID:8278548
A:Accession: PQ0688
A:Molecule type: protein
A:Residues: 1-20 <OBO>
C:Keywords: chloroplast; photosynthesis; photosystem I

Alignment Scores:

Pred. No.:	4.14e+04	Length:	20
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.81%	Indels:	0
DB:	2	Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) x PQ0688 (1-20)

OY 209 GAAGCGCGCGCGCA 195
DB 3 GluAlaAlaProPro 7

Search completed: July 19, 2004, 12:16:31

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 19, 2004, 12:00:12 ; Search time 20 Seconds
(without alignments)
2811.788 Million cell1 updates/sec

Title: US-10-023-182-1_COPY_54_593
Perfect score: 180
Sequence: 1 ATGCAGGCCGAGGCCGCGGCG.....CTCCCTCAGGCGAGAGCGCGC 540

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 141681 seqs, 52070155 residues

Word size: 1

Total number of hits satisfying chosen parameters: 8378

Minimum DB seq length: 5
Maximum DB seq length: 50

Post-processing: listing first 45 summaries

Command line parameters:
MODEL=frame+n2p model -DEV=xlp
O=/cgn2.1/USFO_spool_p/US10023182/runat_19072004_125307_4276/app_query.fasta_1.711
-DB=SwissProt 42 -OFMT=fasta -SUFFIX=011.rsp -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=011go -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=45 -MODE=LOCAL
-OUTMT=ptlo -NORM=ext -HEAPSIZE=500 -MINLEN=5 -MAXLEN=50
-USER=US10023182 @CGN 1 1 20 @runat_19072004_125307_4276 -NCP=6 -ICPU=3
-NO MMAP -LARGEOUERY -NEG SCORES=0 -MATT -DSFBLCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THRCADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
C 1	6	3.4	32 1	HCYC CHEDE
C 2	6	3.4	33 1	RUGA_RANRU
C 3	6	3.4	36 1	SCK2_CENIM
C 4	6	3.4	41 1	C032_LOCM1
C 5	5	2.8	11 1	BPP_AKHP
C 6	5	2.8	14 1	UHAI_CANFA
C 7	5	2.8	18 1	SODM_MYCHA
C 8	5	2.8	19 1	COX4_ONCMY
C 9	5	2.8	19 1	PSAE_UCUSA
C 10	5	2.8	21 1	CAKT_CONTU
C 11	5	2.8	25 1	ANDT_ANDAV
C 12	5	2.8	25 1	ATP0_SPIOL
C 13	5	2.8	26 1	DHAB_AMEME
C 14	5	2.8	26 1	PSBO_PINPS
C 15	5	2.8	27 1	CKKR_CONRA
C 16	5	2.8	27 1	GRP_CHICK
C 17	5	2.8	30 1	SCK2_TITSE
C 18	5	2.8	30 1	Y161_TREPA

19	5	2.8	31 1	PRT3_CLOPA	P02337 clupea pall
C 20	5	2.8	31 1	TXA3_PARAC	P09949 parascyoni
C 21	5	2.8	32 1	OVOS_ANAPL	P20739 anas platyr
C 22	5	2.8	33 1	PETW_SYMBL	O8d15 synechococ
C 23	5	2.8	35 1	HMWC_DESGI	P28588 desulfovibr
C 24	5	2.8	35 1	PSBY_CVAME	O85g61 cyanidiorch
C 25	5	2.8	36 1	IAA_STRAV	P04082 streptomyc
C 26	5	2.8	36 1	MPG2_DACGL	O41183 dactylis gl
C 27	5	2.8	36 1	PYY_MYOSC	P06641 myoxocephal
C 28	5	2.8	37 1	P133_BOVIN	P12260 bos taurus
C 29	5	2.8	37 1	PSBY_CVACA	O19893 cyanidium c
C 30	5	2.8	37 1	SCK1_TITDI	P59923 titylus disc
C 31	5	2.8	37 1	SCKA_TITSE	P46114 titylus serr
C 32	5	2.8	38 1	CU47_LACCU	P03223 lactobacill
C 33	5	2.8	38 1	EXE1_HELSU	P04203 heloderma s
C 34	5	2.8	38 1	R123_PINCO	P49168 pinus conto
C 35	5	2.8	39 1	EXE3_HELHO	P20399 heloderma h
C 36	5	2.8	40 1	MSDB_DROME	Q9vb17 drosophila
C 37	5	2.8	40 1	Y041_TREPA	O83082 treponema p
C 38	5	2.8	42 1	RLA2_WHEAT	P05390 triticum ae
C 39	5	2.8	42 1	COA2_XANCP	O07482 xanthomonas
C 40	5	2.8	43 1	CRC6_CANPG	P81585 cancer pagu
C 41	5	2.8	43 1	LCCC_LETME	P81053 leucomiscoc
C 42	5	2.8	43 1	NLTP_RAPSA	P29420 rapanus sa
C 43	5	2.8	43 1	PSBY_SYNPS	P59908 synechococ
C 44	5	2.8	43 1	SBOA_BACSU	O07623 bacillus su
C 45	5	2.8	44 1	COAB_BPYXF	P03622 bacterioph

ALIGNMENTS

RESULT 1
HCYC CHEDE STANDARD; PRT; 32 AA.
ID P83172;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hemocyanin C chain (Fragment).
OS Cheraex destructor (Yabbie).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eularyotia; Metazoa; Arthropoda; Decapoda; Ploceymata; Astacidea;
OC Parastacoidae; Parastacidae; Cheraex.
OX NCBI_Taxid=6723;
RN [1]
RP SEQUENCE.
RC TISSUE=Hemolymph; PubMed=2620501;
RX MEDLINE=90151075; Sierdsema S.J., Beintema J.J.;
RA Neuteboom B., Sierdsema S.J., Beintema J.J.;
RT "The relationship between N-terminal sequences and immunological
characterization of crustacean hemocyanins.";
RL Comp. Biochem. Physiol. 94B:587-592(1989).
CC -1- FUNCTION: Hemocyanins are copper-containing oxygen carriers
occurring freely dissolved in the hemolymph of many mollusks and
arthropods.
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- TISSUE SPECIFICITY: Hemolymph.
CC -1- SIMILARITY: Belongs to the tyrosinase family. Hemocyanin
subfamily.
DR GO: GO:0005576; C:extracellular; ISS.
DR GO: GO:0005344; F:oxygen transporter activity; IDA.
DR GO: GO:0015671; P:oxygen transport; TAS.
KM Transport; Oxygen transport; Copper; Hemolymph.
FT UNSURE 6
FT NON_TER 32
SQ SEQUENCE 32 AA; 3513 MW; E7FC5E40207B4178 CRC64;

Alignment Scores:
Pred. No.: 2.32e+03 length: 32
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0

```
DB: 1 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x HCYC_CHEDE (1-32)
QY 350 GGAGCGGTGGGGCATCC 333
Db |||||||||||||||
2 GlyserglylAlaser 7

RESULT 2
RUGA_RANRU STANDARD; PRT; 33 AA.
ID P80954;
AC 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Rugosin A.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
NCBI_TaxID=8410;
RN [1]
RP SEQUENCE.
RC TISSUE=skin secretion;
RX MEDLINE=95336450; PubMed=7612013;
RA Suzuki S., Ohe Y., Kagegawa T., Tatemoto K.;
RT "Isolation and characterization of novel antimicrobial peptides,
RL rugosins A, B and C, from the skin of the frog, Rana rugosa.";
RL Biochem. Biophys. Res. Commun. 212:249-254(1995).
CC -!- FUNCTION: Has antibacterial activity against Gram-positive
CC bacteria.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the brevinin family.
KW Amphibian defense peptide; Antibiotic.
FT DISULFID 27 33
SQ SEQUENCE 33 AA; 3440 MW; E41DA4CF3916C4C CRC64;

Alignment Scores:
Pred. No.: 2.31e+03 Length: 33
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
Gaps: 0
DB: 1

US-10-023-182-1_COPY_54_593 (1-540) x RUGA_RANRU (1-33)
QY 54 TGGGCATCATGATGCC 37
Db |||||||||||||||
9 TrpAlaIleSerIleXla 14

RESULT 3
SCR2_CENLM STANDARD; PRT; 36 AA.
ID P59848;
AC 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hongotoxin 2 (HGTX2) (Fragment).
OS Centruroides limbatus (Scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butioidae; Butiidae; Centruroides.
NCBI_TaxID=244936;
RN [1]
RP SEQUENCE.
RX MEDLINE=98112806; PubMed=9446567;
RA Koschak A., Bugianesi R.M., Mitterdorfer J., Kaczorowski G.J.,
RA Garcia M.L., Knaus H.-G.;
RT "Subunit composition of brain voltage-gated potassium channels
RT determined by hongotoxin-1, a novel peptide derived from Centruroides
RT limbatus venom.";
RT J. Biol. Chem. 273:2639-2644(1998).
CC -!- FUNCTION: Potent selective inhibitor of Kv1 voltage-gated
```

```
CC potassium channels (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- SIMILARITY: Belongs to the short scorpion toxin family. Potassium
CC channel inhibitor subfamily.
DR PROSITE, PS01139; SCOP_SHORT_TOXIN, 1.
KW Toxin; Neurotoxin; Ionic channel inhibitor;
KW Potassium channel inhibitor.
FT NON TER 36 36
SQ SEQUENCE 36 AA; 3946 MW; A9D585FC06312E16 CRC64;

Alignment Scores:
Pred. No.: 2.28e+03 Length: 36
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
Gaps: 0
DB: 1

US-10-023-182-1_COPY_54_593 (1-540) x SCR2_CENLM (1-36)
QY 475 ACAGGGAAGCTGCTGA 458
Db |||||||||||||||
21 ThrGlySerAlaAlaGly 26

RESULT 4
CU32_LOCM1 STANDARD; PRT; 41 AA.
ID CU32_LOCM1
AC P11736;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DE 01-FEB-1996 (Rel. 33, Last annotation update)
DE Cuticle protein 32 (LM-32) (LM-ACP 32) (Fragment).
OS Locusta migratoria (Migratory locust).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygora;
OC Neoptera; Orthopteroidea; Orthoptera; Caelifera; Acridoidea;
OC Acridoidea; Acrididae; Oedipodinae; Locusta.
NCBI_TaxID=7004;
RN [1]
RP SEQUENCE.
RX MEDLINE=86108304; PubMed=3943519;
RA Hoejrup P., Andersen S.O., Roepstorff P.;
RT "Isolation, characterization, and N-terminal sequence studies of
RT cuticular proteins from the migratory locust, Locusta migratoria.";
RL Eur. J. Biochem. 154:153-159(1986).
CC -!- FUNCTION: Component of the cuticle of migratory locust which
CC contains more than 100 different structural proteins.
CC -!- DOMAIN: The tetrapeptide (A-A-P-(AV)) repeats found throughout the
CC protein are also present in many proteins constituting the
CC protective envelope of other species.
DR PIR, E24802; E24802.
KW Structural protein; Cuticle; Repeat.
FT REPEAT 17 20 1.
FT REPEAT 25 28 2.
FT REPEAT 31 34 3.
FT REPEAT 38 41 4.
FT NON TER 41 41
SQ SEQUENCE 41 AA; 3697 MW; 119A8AF4EB94EAF4 CRC64;

Alignment Scores:
Pred. No.: 2.25e+03 Length: 41
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
Gaps: 0
DB: 1

US-10-023-182-1_COPY_54_593 (1-540) x CU32_LOCM1 (1-41)
QY 158 GCCCTGCTGCCCTGCG 141
Db |||||||||||||||
15 AlaLeuAlaAlaProAla 20
```


RESULT 5
BPP_AGKHP
ID_BPP_AGKHP STANDARD; PRT; 11 AA.
AC P04562;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bradykinin-potentiating peptide (Angiotensin-converting enzyme inhibitor).
OS Agkistrodon halys pallas (Chinese water moccasin) (Gloydus halys pallas).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidodonta; Squamata; Scleroglossa; Serpentes; Colubroidea; Viperidae; Crotalinae; Gloydius.
OC NCBI_TaxID=8714;
OX NCBI_TaxID=8714;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=86177022; PubMed=3008123;
RA Chi C.-W., Wang S.-Z., Xu L.-G., Wang M.-Y., Lo S.-S., Huang W.-D.;
RT "Structure-function studies on the bradykinin potentiating peptide from Chinese snake venom (Agkistrodon halys pallas).";
RL Peptides 6 Suppl. 3:339-342(1985).
CC -1- FUNCTION: This peptide both inhibits the activity of the angiotensin-converting enzyme and enhances the action of bradykinin by inhibiting the kinases that inactivate it.
CC It acts as an indirect hypotensive agent.
DR PIR: J00002; XAVIBH.
KM Hypotensive agent; Pyrrolidone carboxylic acid.
FT MOD RES 1 PYRROLIDONE CARBOXYLIC ACID.
SQ SEQUENCE 11 AA; 1112 MW; 30BABF1277686777 CRC64;
Alignment Scores:
Pred. No.: 2.48e+04 Length: 11
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x BPP_AGKHP (1-11)
QY 249 CGGCCCTGGCCCC 235
Db 3 ArgProProGlyPro 7
RESULT 6
UHAI_CANFA
ID_UHAI_CANFA STANDARD; PRT; 14 AA.
AC P99503;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Unknown protein from 2D-page of heart tissue (Spot 11) (Fragment).
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OC NCBI_TaxID=9615;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=98163340; PubMed=9504812;
RA Dunn M.J., Corbett J.M., Wheeler C.H.;
RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of dog heart proteins.";
RL Electrophoresis 18:2795-2802(1997).
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 4.3, its MW is: 19.6 kDa.
DR HSC-2DPAGE; P99503; DOG.
FT NON TER 14
SQ SEQUENCE 14 AA; 1149 MW; 3D9238888D8668C7 CRC64;
Alignment Scores:

Pred. No.: 2.41e+04 Length: 14
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x UHAI_CANFA (1-14)
QY 152 GCTGCCCCGGCCCC 138
Db 5 AlaAlaProAlaPro 9
RESULT 7
SODM_MYCHA
ID_SODM_MYCHA STANDARD; PRT; 18 AA.
AC P80582;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Superoxide dismutase [Mn] (EC 1.15.1.1) (Fragment).
GN SODA OR SOD.
OS Mycobacterium habana.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.
OC NCBI_TaxID=1784;
OX NCBI_TaxID=1784;
RN [1]
RP SEQUENCE.
RC STRAIN=TMC 5135;
RX MEDLINE=9626709; PubMed=8704977;
RA Biehl D., Mehrotra J., Dhindsa M.S., Singh N.B., Sinha S.;
RT "A major T-cell-inducing cytosolic 23 kDa protein antigen of the vaccine candidate Mycobacterium habana is superoxide dismutase.";
RL Microbiology 142:1375-1383(1996).
CC -1- FUNCTION: Destroys radicals which are normally produced within the cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 manganese ion per subunit (By similarity).
CC -1- SUBUNIT: Homodimer (Probable).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase family.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; sodfe; 1.
DR PROSITE: PS00088; SOD_MN; PARTIAL.
KM Oxidoreductase; Metal-binding; Manganese.
FT NON TER 18
SQ SEQUENCE 18 AA; 1883 MW; A4161A3DAC93F710 CRC64;
Alignment Scores:
Pred. No.: 2.33e+04 Length: 18
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.78% Indels: 0
Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x SODM_MYCHA (1-18)
QY 157 GCTTGGGGCCGGGGA 171
Db 14 AlaSerGlyProGly 18
RESULT 8
COX4_ONCMY
ID_COX4_ONCMY STANDARD; PRT; 19 AA.
AC P80327;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cytochrome c oxidase polypeptide IV (EC 1.9.3.1) (Fragments).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Procaracanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxId=8022;
RN [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and VIIa
of cytochrome c oxidase isolated from rainbow trout.";
RL Eur. J. Biochem. 221:1111-1116(1994).
CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide
chains of cytochrome c oxidase, the terminal oxidase in
mitochondrial electron transport.
CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
c + 2 H(2)O.
CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -1- SIMILARITY: Belongs to the cytochrome c oxidase IV family.
DR PIR; S43624; S43624.
KW Oxidoreductase; Inner membrane; Mitochondrion.
FT NON_CONS 9 10
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 1963 MW; 9280E1DBEC77987B CRC64;

Alignment Scores:
Pred. No.: 2.32e+04 Length: 19
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
Gaps: 0
DB: 1
US-10-023-182-1_COPY_54_593 (1-540) x COX4_ONCMY (1-19)
QY 282 CATGGCGAGCTAGAA 268
DB 3 HSG1G1uvalGlu 7

RESULT 9
PSAE_CUCSA STANDARD; PRT; 19 AA.
ID PSAE_CUCSA
AC P42047;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Photosystem I reaction center subunit IV (Psl-E) (Photosystem I 19.5
kDa protein) (Psl I subunit 6) (Fragment).
GN PSAE.
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucotyledons; Cucurbitales; Cucurbitaceae; Cucumis.
OX NCBI_TaxId=3659;
RN [1]
RP SEQUENCE.
RC TISSUE=Cotyledon;
RX MEDLINE=91355209; PubMed=1883835;
RA Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;
RT "Characterization of genes that encode subunits of cucumber Psl I
complex by N-terminal sequencing.";
RL Biochim. Biophys. Acta 1059:141-148(1991).
CC -1- FUNCTION: Stabilizes the interaction between PslC and the Psl
core, assists the docking of the ferredoxin to Psl and interacts
with ferredoxin-NADP oxidoreductase (By similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
CC -1- SIMILARITY: Belongs to the psae family.
DR PIR; G56819; G56819.
KW Photosynthesis; Photosystem I; Chloroplast; Thylakoid; Membrane.
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 1810 MW; A33E8BDD089FB738 CRC64;

Alignment Scores:
Pred. No.: 2.32e+04 Length: 19

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
Gaps: 0
DB: 1
US-10-023-182-1_COPY_54_593 (1-540) x PSAE_CUCSA (1-19)
QY 209 GAGCGGCGCGCCA 195
DB 3 Glu1Aa1a1aProPro 7

RESULT 10
CKKT_CONTU STANDARD; PRT; 21 AA.
ID CKKT_CONTU
AC P17684;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Conantokin-T (Con-T).
OS Conus tulipa (Fish-hunting cone snail) (Tulip cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxId=6495;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=90202866; PubMed=2180939;
RA Haack J.A., Rivier J.E., Parks T.N., Mena E.E., Cruz L.J.,
RA Olivera B.M.;
RT "Conantokin-T. A gamma-carboxyglutamate containing peptide with
N-methyl-D-aspartate antagonist activity.";
RL J. Biol. Chem. 265:6025-6029(1990).
RN [2]
RP FUNCTION.
RX MEDLINE=90327072; PubMed=2165278;
RA Yoshikami D.;
RT Unpublished results, cited by:
RL Olivera B.M., Rivier J.E., Clark C., Ramilo C.A., Corpuz G.P.,
RL Abogadie F.C., Mena E.E., Woodward S.R., Hillyard D.R., Cruz L.J.,
RL Science 249:257-263(1990).
RN [3]
RP STRUCTURE BY NMR.
RX MEDLINE=97388901; PubMed=9247135;
RA Warder S.E., Chen Z., Zhu Y., Proxok M., Castellino F.J., Ni F.;
RT "The NMR solution structure of the NMDA receptor antagonist,
RL conantokin-T, in the absence of divalent metal ions.";
RN FEBS Lett. 411:19-26(1997).
RN [4]
RP STRUCTURE BY NMR.
RX MEDLINE=97153002; PubMed=8999936;
RA Skjaerbaek N., Nielsen K.T., Lewis R.J., Alewood P.F., Craik D.J.;
RT "Determination of the solution structures of conantokin-G and
RL conantokin-T by CD and NMR spectroscopy.";
RN J. Biol. Chem. 272:2291-2299(1997).
CC -1- FUNCTION: Induces sleep-like symptoms in young mice and
hyperactivity in older mice. Inhibits N-methyl-D-aspartate (NMDA)
receptor-mediated calcium influx in central nervous system
neurons.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- SIMILARITY: Belongs to the conantokin family.
DR PIR; A35225; A35225.
DR PDB; 1ONT; 04-SEP-97.
KW Toxin; Vitamin K; Gamma-carboxyglutamic acid; Calcium; Amidation;
3D-structure.
FT MOD_RES 3 3 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 4 4 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 10 10 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 14 14 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 21 21 AMIDATION.
SQ SEQUENCE 21 AA; 2509 MW; 7F7B893AC4842C38 CRC64;

Alignment Scores:

Pred. No.: 2.29e+04 Length: 21
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x CKKT_CONTU (1-21)

QY 529 CTGAGGAGGCTGAG 515

DB 12 LeuArgGluAlaGlu 16

RESULT 11

ANDT ANDAU STANDARD; PRT; 25 AA.
AC P56684; P81616;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Androctonus.
OS Androctonus australis (Sahara scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butiidae; Butiidae; Androctonus.
OX NCBI_Taxid=6858;

RN [1] SEQUENCE, CHARACTERIZATION, AND SYNTHESIS.

RP STRAIN=Hector; TISSUE=Hemolymph;

RX MEDLINE=97094646; PubMed=8939880;

RA Eshet-Sabatie L., Loew D., Goyffon M., Fehlbaum P., Hoffmann J.A.,
van Doorselaer A., Bulet P.; Goyffon M., Fehlbaum P., Hoffmann J.A.,
"Characterization of novel cysteine-rich antimicrobial peptides from
scorpion blood.";

RT J. Biol. Chem. 271:29537-29544(1996).

RN [2] SYNTHESIS OF D-AMINO ACID ENANTIOMER, AND CHARACTERIZATION.

RP STRAIN=Hector;

RX MEDLINE=20115101; PubMed=10642525;

RA Heru C., Leticier L., Oren Z., Hoffmann J.A., Shai Y.,
"Androctonin, a hydrophilic disulphide-bridged non-haemolytic
anti-microbial peptide: a plausible mode of action.";

RL Biochem. J. 345:653-664(2000).

RN [3] STRUCTURE BY NMR.

RP STRAIN=Hector;

RX MEDLINE=20025109; PubMed=10563585;

RA Mandard N., Sy D., Maufrais C., Bonmatin J.M., Bulet P., Heru C.,
Vovelle F.;
"Androctonin, a novel antimicrobial peptide from scorpion Androctonus
australis: solution structure and molecular dynamics simulations in
the presence of a lipid monolayer.";

RL J. Biomol. Struct. Dyn. 17:367-380(1999).

CC -1- FUNCTION: Active against both bacteria (Gram-positive and Gram-
negative) and filamentous fungi. Acts on the membrane of the
bacterial cells. It destabilize a membrane by modifying its
properties.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- MASS SPECTROMETRY: MW=3076.7; METHOD=Electrospray.

KW Antibiotic; Fungicide; 3D-structure.

FT DISULFID 4 20
FT DISULFID 10 16
FT STRAND 6 9
FT STRAND 17 20
SQ SEQUENCE 25 AA; 3081 MW; D4183D6BA5A50AA CRC64;

Alignment Scores:

Pred. No.: 2.24e+04 Length: 25
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.78% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x ANDT_ANDAU (1-25)

QY 102 AGGAGGCGGCTGC 116

DB 12 ArgArgGlyGlyCys 16

RESULT 12

ATP0_SPIOL STANDARD; PRT; 25 AA.
ID ATP0_SPIOL
AC P80082;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ATP synthase alpha chain, mitochondrial (EC 3.6.3.14)
DE (Fragment).
GN ATPA.
OS Spinacia oleracea (Spinach).

OC Mitochondrion.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.

OX NCBI_Taxid=3562;

RN [1] SEQUENCE.

RP STRAIN=cv. Medania; TISSUE=leaf mesophyll;

RX MEDLINE=92209531; PubMed=1313368;

RA Hamaus B., Glaeser E.;
"Plant mitochondrial FOF1 ATP synthase. Identification of the
individual subunits and properties of the purified spinach leaf
mitochondrial ATP synthase.";

RL Eur. J. Biochem. 205:409-416(1992).

CC -1- FUNCTION: Produces ATP from ADP in the presence of a proton
gradient across the membrane. The alpha chain is a regulatory
subunit.CC -1- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (in) = ADP + phosphate +
H(+) (out).CC -1- SUBUNIT: F-type ATPases have 2 components, CF(1) - the catalytic
core - and CF(0) - the membrane proton channel. CF(1) has five
subunits: alpha(3), beta(3), gamma(1), delta(1), epsilon(1). CF(0)

CC has three main subunits: a, b and c.

CC -1- SUBCELLULAR LOCATION: Mitochondrial.

DR PIR; S21204; S21204.

DR InterPro; IPR000194; ATPase_a/bcentre.

DR PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.

KW ATP synthase; CF(1); Hydrogen ion transport;
Hydrolyase; ATP-binding; Mitochondrion.FT NON TER 25
SQ SEQUENCE 25 AA; 2904 MW; 1B1486BBD1A650D CRC64;

Alignment Scores:

Pred. No.: 2.24e+04 Length: 25
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.78% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x ATP0_SPIOL (1-25)

QY 116 CCACGCGCGCAGAG 130

DB 5 ProArgAlaAlaGlu 9

RESULT 13

DHAB_AMYME STANDARD; PRT; 26 AA.
ID DHAB_AMYME
AC P80472;

DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)

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DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Aldheyde dehydrogenase, beta chain (EC 1.2.99.3) (ALDH) (Fragment).
OS Amycolatopsis methanolica.
OC Bacteria; Actinobacteriae; Actinomycetales;
OC Pseudonocardineae; Pseudonocardiaceae; Amycolatopsis.
OX NCBI_TaxID=1814;
RN [1]
RP SEQUENCE.
RC STRAIN=NCIB 11946;
RC MEDLINE=96140591; PubMed=8554333;
RA Kim S.W., Luykx D.M.A.M., de Vries S., Duine J.A.;
RT "A second molybdoprotein aldehyde dehydrogenase from Amycolatopsis
RT methanolica NCIB 11946."
RL Arch. Biochem. Biophys. 325:1-7(1996).
CC -1- CATALYTIC ACTIVITY: An aldehyde + acceptor + H(2)O = a carboxylate
CC + reduced acceptor.
CC -1- COFACTOR: Molybdenum.
CC -1- SUBUNIT: Heterotrimer composed of an alpha, a beta and a gamma
CC chain.
KW Oxidoreductase; Molybdenum.
FT NON_TER 26
SQ SEQUENCE 26 AA; 2834 MW; 209C75D48FA7B35C CRC64;

Alignment Scores:
Pred. No.: 2.23e+04 Length: 26
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0
RN [1]

US-10-023-182-1_COPY_54_593 (1-540) x DHAB_AMYME (1-26)
QY 161 GAGCCCTTGTCGCC 147
Db |||||
16 GluAlaLeuAlaAla 20

RESULT 14
PSBO_PINPS STANDARD; PRT; 26 AA.
AC P81655;
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Oxygen-evolving enhancer protein 1 (OEE1) (33 kDa subunit of oxygen
DE evolving system of photosystem II) (33 kDa thylakoid membrane
DE protein) (Fragments).
GN PSBO.
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=71647;
RN [1]
RP SEQUENCE.
RC TISSUE=Needle;
RC MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubos C., Bahman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins."
RL Electrophoresis 20:1098-1108(1999).
CC -1- FUNCTION: Stabilizes the manganese cluster which is the primary
CC site of water splitting (By similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane; associated
CC with the photosystem II complex (By similarity).
CC -1- INDUCTION: By water stress.
CC -1- MISCELLANEOUS: On the 2D-gel, the determined pI of this protein
CC (spot N146) is: 5.3, its Mw is: 29 kDa.
CC -1- SIMILARITY: Belongs to the psdO family.
KW Photosynthesis; Photosystem II; Chloroplast; Thylakoid; Membrane;
Manganese.
FT NON_CONS 9 10
FT NON_TER 26 26

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SQ SEQUENCE 26 AA; 2641 MW; C5635997B460842F CRC64;

Alignment Scores:
Pred. No.: 2.23e+04 Length: 26
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.78% Indels: 0
DB: 1 Gaps: 0
RN [1]

US-10-023-182-1_COPY_54_593 (1-540) x PSBO_PINPS (1-26)
QY 25 GGGGTTGACGGCGC 39
Db |||||
10 GlyGlySerThrGly 14

RESULT 15
CKXR_CONRA STANDARD; PRT; 27 AA.
AC P58806;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Conantokin-R (Con-R).
OS Conus radiatus (Rayed cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OX NCBI_TaxID=61198;
RN [1]
RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RC MEDLINE=20072842; PubMed=10604979;
RA White H.S., McCabe R.T., Armstrong H., Donevan S.D., Cruz L.J.,
RA Abogadie F.C., Torres J., Rivier J.E., Patzmann I., Hollmann M.,
RA Olivera B.M.;
RT "In vitro and in vivo characterization of conantokin-R, a selective
RT NMDA receptor antagonist isolated from the venom of the fish-hunting
RT snail Conus radiatus."
RL J. Pharmacol. Exp. Ther. 292:425-432(2000).
CC -1- FUNCTION: Induces sleep-like symptoms in young mice. Inhibits
CC N-methyl-D-aspartate (NMDA) receptor-mediated calcium influx in
CC central nervous system neurons.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: Mw=3098.
CC -1- SIMILARITY: Belongs to the conantokin family.
KW Toxin; Vitamin K; Gamma-carboxyglutamic acid; Calcium.
FT DISULFD 21 25 PROBABLE.
FT MOD_RES 3 3 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 4 4 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 11 11 GAMMA-CARBOXYGLUTAMIC ACID.
FT MOD_RES 15 15 GAMMA-CARBOXYGLUTAMIC ACID.
SQ SEQUENCE 27 AA; 2924 MW; 2DD1C3AD7DB88C53 CRC64;

Alignment Scores:
Pred. No.: 2.22e+04 Length: 27
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.78% Indels: 0
DB: 1 Gaps: 0
RN [1]

US-10-023-182-1_COPY_54_593 (1-540) x CKXR_CONRA (1-27)
QY 304 GCAAGCTGGCCCGC 318
Db |||||
10 AlaGluLeuAlaArg 14

RESULT 16
GRP_CHICK STANDARD; PRT; 27 AA.
AC P01295;

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DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gastrin-releasing peptide (GRP) (Proventricular peptide) [Contains:
DE Neuromedin C (GRP-10)].
GN GRP.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
NCBI_TaxID=9031;
RN [1]
RP SEQUENCE.
RX MEDLINE=8164953; PubMed=7215543;
RA McDonald T.J., Joernvall H., Ghatei M., Bloom S.R., Mutt V.;
RT "Characterization of an avian gastrin (proventricular) peptide having
RT sequence homology with the porcine gastrin-releasing peptide and the
RT amphibian peptides bombesin and alytesin.";
RL FEBS Lett. 122:45-48(1980).
RN [2]
RP SEQUENCE.
RX MEDLINE=90122926; PubMed=2297533;
RA Campbell B.J., Young J., Dimaline R., Dockray G.J.;
RT "Isolation, sequence and biosynthetic significance of a novel
RT fragment of gastrin-releasing peptide from chicken proventriculus.";
RL Biochim. Biophys. Acta 1048:66-71(1990).
CC -1- FUNCTION: GRP stimulates gastrin release as well as other
CC gastrointestinal hormones.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the bombesin/neuromedin B/ratanensin
CC family.
DR PIR: A01563; RCHGA.
DR InterPro: IPR000874; Bombesin.
DR Pfam: PF02044; Bombesin_1.
DR PROSITE: PS00257; BOMBESIN_1.
KW Bombesin family; Amidation.
FT PEPTIDE 18 27 NEUROMEDIN C.
FT MOD_RES 27 27 AMIDATION.
SQ SEQUENCE 27 AA; 2842 MW; 3C121D011B0551C7 CRC64;
Alignment Scores:
Pred. No.: 2.22e+04 Length: 27
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x GRP_CHICK (1-27)
QY 259 GGGGCTCTCGGCC 245
DB 6 GlyGlySerProAla 10
RESULT 17
SCK2_TITSE STANDARD; PRT; 30 AA.
ID_SCK2_TITSE
AC P08816;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Toxin II-9 (Fragment).
OS Tityus serrulatus (Brazilian scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butiidae; Butiidae; Tityus.
NCBI_TaxID=6887;
RN [1]
RP SEQUENCE.
RX TISUB-Venom;
RA Posanti L.D., Martin B.M., Svendsen I.;
RT "The primary structure of noxiustoxin, A K channel blocking peptide,
RT purified from the venom of the scorpion Centruroides noxius
RT Hoffmann.";

RL Carlsberg Res. Commun. 47:285-289(1982).
CC -1- FUNCTION: Blocker for calcium-activated potassium channels.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- PTM: Three disulfide bonds are present. One is indicated here.
CC -1- SIMILARITY: Belongs to the short scorpion toxin family. Potassium
CC channel inhibitor subfamily.
DR HSSP: P24662; 2KTX.
DR InterPro: IPR001947; Scorpion_toxins.
DR Pfam: PF00451; toxin_2; 1.
DR ProDom: PD003586; Scorpion_toxins; 1.
DR PROSITE: PS01138; SCOR_SHORT_TOXIN; PARTIAL.
KW Toxin; Neurotoxin; Ionic channel inhibitor;
KW Potassium channel inhibitor.
FT DISULFID 7 28 BY SIMILARITY.
FT VARIANT 21 21 I -> F.
FT VARIANT 29 29 V -> M.
FT NON_TER 30 30
SQ SEQUENCE 30 AA; 3164 MW; 1919E6EDB136DFE CRC64;
Alignment Scores:
Pred. No.: 2.19e+04 Length: 30
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x SCK2_TITSE (1-30)
QY 472 GGAAGCTGCTGGA 458
DB 22 GlyGlyAlaGly 26
RESULT 18
ID_Y161_TREPA STANDARD; PRT; 30 AA.
AC 083196;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein TP0161.
GN TP0161.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutron G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardam J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utecherack T.,
RA McDonald L., Artach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandersky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
RL Science 281:375-388(1998).
CC -----
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CC -----
DR EMBL: AE001200; AAC65153.1; -.
DR PIR: G71359; G71359.
DR TIGR: TP0161; -.
KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 30 AA; 3259 MW; 4B9A413A5498D15F CRC64;
 Alignment Scores:
 Pred. No.: 2.19e+04 Length: 30
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.81% Indels: 0
 DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Y161_TREPA (1-30)
 QY 148 CCCCTGCCGCCCGCG 134
 Db 8 ProteArgProgly 12

RESULT 19
 PRT3_CLUPA STANDARD; PRT; 31 AA.
 AC P02337;
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Protamine YI (Clupeine YI).
 OS Clupea pallasii (Pacific herring), and
 OS Clupea harengus (Atlantic herring);
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Clupeomorpha; Clupeidae;
 OC Clupea.
 OX NCBI_TaxID=30724, 7950;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=C.pallasii;
 RX MEDLINE=72323107; PubMed=4664741;
 RA Suzuki K., Ando T.;
 RT "Studies on protamines. XVII. The complete amino acid sequence of
 RT clupeine YI.";
 RL J. Biochem. 72:1433-1446 (1972).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=C.harengus;
 RA Chang W.J., Mukeshina M., Ishii S., Nakahara C., Ando T.;
 RL Submitted (Aug-1970) to the PIR data bank.
 CC -1- FUNCTION: Protamines substitute for histones in the chromatin of
 CC sperm during the haploid phase of spermatogenesis. They compact
 CC sperm DNA into a highly condensed, stable and inactive complex.
 CC -1- SUBCELLULAR LOCATION: Nuclear.
 CC -1- TISSUE SPECIFICITY: Testis.
 DR PIR; A37577; CLHRIA.
 DR PIR; A38051; CLHRI1.
 KW Chromosomal protein; Nucleosome core; Spermatogenesis; DNA-binding;
 KW Testis; DNA condensation; Nuclear protein.
 SQ SEQUENCE 31 AA; 4112 MW; BDC9A140FF7F819 CRC64;

Alignment Scores:
 Pred. No.: 2.18e+04 Length: 31
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.78% Indels: 0
 DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x PRT3_CLUPA (1-31)
 QY 165 GCCGGAGAGGCGC 179
 Db 26 AlaGlyArgArgArg 30

RESULT 20
 TXA3_PARAC STANDARD; PRT; 31 AA.
 ID TXA3_PARAC
 AC P09949;
 DT 01-MAR-1989 (Rel. 10, Created)

DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)
 DE Neurotoxin III homolog (PA-TX).
 OS Parascyonia actinostoloides (Sea anemone) (Entacmea quadricolor).
 OC Eukaryota; Metazoa; Cnidaria; Anthozoa; Zoantharia; Actinaria;
 OC Nymphaeae; Actiniidae; Entacmea.
 OX NCBI_TaxID=6118;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Cnidoblast;
 RX MEDLINE=85257626; PubMed=2862037;
 RA Nishida S., Fujita S., Marashina A., Satake M., Tamiya N.;
 RT "Amino acid sequence of a sea anemone toxin from Parascyonia
 RT actinostoloides.";
 RL Eur. J. Biochem. 150:171-173 (1985).
 CC -1- FUNCTION: Binds specifically to the sodium channel.
 CC -1- SUBCELLULAR LOCATION: Secreted; cndocyst.
 CC -1- PTM: Contains four disulfide bonds.
 CC -1- SIMILARITY: Belongs to the sea anemone short toxin family.
 DR PIR; A25210; A25210.
 KW Toxin; Neurotoxin; Ionic channel inhibitor; Sodium channel inhibitor;
 KW Cndocyst.
 SQ SEQUENCE 31 AA; 3123 MW; 39CBE84131B68A37 CRC64;

Alignment Scores:
 Pred. No.: 2.18e+04 Length: 31
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.81% Indels: 0
 DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x TXA3_PARAC (1-31)
 QY 153 TGCTGCCCGCGCGC 139
 Db 7 CysCysProCysAla 11

RESULT 21
 OVOS_ANAPL STANDARD; PRT; 32 AA.
 AC P20739;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last annotation update)
 DE Ovocystin (Ovomacroglobulin) (Fragment).
 OS Anas platyrhynchos (Domestic duck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=8839;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=88005157; PubMed=3653403;
 RA Nagase H., Brew K.;
 RT "Amino acid sequence of a 32-residue region around the thiol ester
 RT site in duck ovocystatin.";
 RL FEBS Lett. 222:83-88 (1987).
 CC -1- FUNCTION: Is able to inhibit all four classes of proteinases by a
 CC unique "trapping" mechanism. This protein has a peptide stretch,
 CC called the 'bait region' which contains specific cleavage sites
 CC for different proteinases. When a proteinase cleaves the bait
 CC region, a conformational change is induced in the protein which
 CC traps the proteinase. The entrapped enzyme remains active against
 CC low molecular weight substrates (activity against high molecular
 CC weight substrates is greatly reduced). Following cleavage in the
 CC bait region a thiolester bond is hydrolyzed and mediates the
 CC covalent binding of the protein to the proteinase.
 CC -1- SUBUNIT: Homotetramer, which consists of two pairs of disulfide-
 CC linked chains.
 CC -1- SIMILARITY: TO OTHER PROTEINS OF THE ALPHA-MACROGLOBULIN FAMILY,
 CC INCLUDING COMPLEMENT COMPONENTS C3, C4, AND C5.
 DR PIR; S00121; S00121.
 DR GO; GO:0017114; F:wide-spectrum protease inhibitor activity; NMS.

DR InterPro: IPR001599; MacroglublnA2.
DR InterPro: IPR008930; Terp_cyc_toroid.
DR Pfam: PF00207; A2M; 1.
DR PROSITE: PS00477; ALPHA_2_MACROGLOBULIN; 1.
KW Serine protease inhibitor; Glycoprotein; Bait region; Thioester bond.
FT NON_TER 1
FT CROSSLINK 27 30 Isoglutaryl cysteine thioester (Cys-Gln).
FT NON_TER 32
SQ SEQUENCE 32 AA; 3472 MW; 7795D67965E28581 CRC64;

Alignment Scores:
Pred. No.: 2.17e+04 Length: 32
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.78* Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x OVOS_ANAPL (1-32)
OY 441 CTCGATCGAGCTCGT 455
Db 17 LeuHsgInLeu 21

RESULT 22
PETM_SYNEL STANDARD; PRT; 33 AA.
AC Q8DJ15:
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome b6-f complex subunit VII (Cytochrome b6f complex subunit
DE PETM).
GN PETM OR TSRI416.
OS Synecchococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synecchococcus.
OX NCBI_TaxID=32046;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP-1;
RX MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneo T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Matanabe A., Iriyuchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the thermophilic cyanobacterium
Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
CC -1- FUNCTION: Cytochrome b6-f complex subunit.
CC -1- SUBCELLULAR LOCATION: Cellular thylakoid membrane-associated (By
CC similarity).
CC -1- SIMILARITY: Belongs to the petM family.
CC -----
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CC -----
DR HAMAP: MF00396; -; 1.
KW Electron Transport; Respiratory chain; Thylakoid; Transmembrane;
KM Complete proteome.
FT TRANSMEM 9
SQ SEQUENCE 33 AA; 3567 MW; BF91F5DB46A9BF89 CRC64;

Alignment Scores:
Pred. No.: 2.17e+04 Length: 33
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.78* Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x PETM_SYNEL (1-33)
OY 156 GGCTCGGCGCGCG 170
Db 19 GlyLeuGlyAlaGly 23

RESULT 23
HMMC_DESGI STANDARD; PRT; 35 AA.
ID HMMC_DESGI
AC P38588;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 01-OCT-1994 (Rel. 34, Last annotation update)
DE High-molecular-weight cytochrome C (Cytochrome CC3) (Fragment).
DE HMC.
GN Desulfovibrio gigas.
OS Desulfovibrio gigas.
OC Bacteria; Proteobacteria; Delta proteobacteria; Desulfovibrionales;
OC Desulfovibrionaceae; Desulfovibrio.
OX NCBI_TaxID=879;
RN [1]
RP SEQUENCE.
RC STRAIN=ATCC 19364 / NCIB 9332;
RX MEDLINE=94307403; PubMed=8034021;
RA Chen L., Pereira M.M., Teixeira M., Xavier A.V., Le Gall J.;
RT "Isolation and characterization of a high molecular weight cytochrome
RT from the sulfate reducing bacterium Desulfovibrio gigas.";
RL FEBS Lett. 347:295-299(1994).
CC -1- FUNCTION: MAY ACT AS AN ELECTRON ACCEPTOR OF THE ENZYME
CC -1- HYDROGENASE OR AS AN ELECTRON DONOR TO RUBREROXIN.
CC -1- SUBUNIT: Homodimer.
CC -1- PTM: MAY BIND 16 HEME GROUPS PER MOLECULE. 14-15 OF THE HEMES ARE
CC LOW-SPIN BIS-HISTIDINYL COORDINATED, AND 1-2, HIGH-SPIN HEMES.
CC -1- SIMILARITY: TO OTHER HIGH-MOLECULAR-WEIGHT CYTOCHROME C.
DR PIR: S46248; S46248.
DR InterPro: IPR000345; Cytc heme BS.
DR PROSITE: PS00190; CYTOCHROME C1 PARTIAL.
KW Electron transport; Sulfate respiration; Heme.
FT NON_TER 35
SQ SEQUENCE 35 AA; 3633 MW; 3883D386F73969ED CRC64;

Alignment Scores:
Pred. No.: 2.15e+04 Length: 35
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81* Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x HMMC_DESGI (1-35)
OY 243 CCGGCGCCCGCATCT 229
Db 3 ProcllyProHlaSer 7

RESULT 24
PSBY_CYAME STANDARD; PRT; 35 AA.
ID PSBY_CYAME
AC Q85G61;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Photosystem II protein Y.
GN PSBY.
OS Cyanidioschyzon merolae (Red alga).
OC Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Cyanidioschyzon.
OX NCBI_TaxID=45157;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=10D;

CC MEDLINE=22639682; PubMed=12755171;
RA Ohta N., Matsuzaki M., Misumi O., Miyajima S.-Y., Nozaki H.,
RA Tanaka K., Shin-I T., Kohara Y., Kuroiwa T.;
RT "Complete sequence and analysis of the plastid genome of the
RT unicellular red alga *Cyanidioschyzon merolae*.";
RL DNA Res. 10:67-77(2003).
CC -1- FUNCTION: Manganese-binding polypeptide with L-arginine
CC metabolizing enzyme activity. Component of the core of photosystem
CC II (By similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
CC -1- SIMILARITY: Belongs to the psbJ family.

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DR EMBL: AB002583; BAC76130.1; -.
DR HAMAP: MF 00717; -; 1.
KW Photosynthesis; Photosystem II; Transmembrane; Thylakoid; Chloroplast.
FT DOMAIN 1 4 LOMENAL (POTENTIAL).
FT TRANSMEM 5 23 POTENTIAL.
FT DOMAIN 24 35 STROMAL (POTENTIAL).
SQ SEQUENCE 35 AA; 3923 MW; F04ADP74B5D34CA CRC64;

Alignment Scores:
Pred. No.: 2.15e+04 Length: 35
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x PSBY_CYAME (1-35)

QY 60 GCCTCCTGGGCCATC 46
DB 16 AAserrpAlaIle 20

RESULT 25
IAA STRAU STANDARD; PRT; 36 AA.
AC P04082; |||||
DT 01-NOV-1986 (Rel. 03, Created)
DT 01-NOV-1986 (Rel. 03, Last sequence update)
DT 01-MAR-1989 (Rel. 10, Last annotation update)
DE Alpha-amylase inhibitor AI-3688 (Fragment).
OS Streptomyces aureofaciens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_Taxid=1894;
RN (1)
RP SEQUENCE.
RC STRAIN=DSM 2790;
RX MEDLINE=85204394; PubMed=2581812;
RA Veresky L., Tripler D.;
RT "Isolation and structure elucidation of an alpha-amylase inhibitor,
RT AI-3688, from Streptomyces aureofaciens.";
RL FEBS Lett. 185:187-190(1985).
CC -1- FUNCTION: INHIBITS MAMMALIAN ALPHA-AMYLASES SPECIFICALLY BUT
CC HAS NO ACTION ON PLANT AND MICROBIAL ALPHA-AMYLASES.
CC -1- MISCELLANEOUS: THIS PROTEIN IS AN EFFECTIVE INHIBITOR OF
CC PANCREATIC ALPHA-AMYLASE, IT IS 5 TIMES LESS EFFECTIVE AGAINST
CC HUMAN SALIVARY AMYLASE.
CC PIR: A01331; WISMAA.
DR HSSP: P01092; 1BVN.
DR InterPro: IPR000833; A_amyase_inhib.
DR Pfam: PF01356; A_amyase_inhib_1.
DR ProDom: PD009058; A_amyase_inhib; 1.
KW Alpha-amylase inhibitor.

FT DISULFID 9 25
FT NON TER 36 36
SQ SEQUENCE 36 AA; 3938 MW; 64A65B321BE3A829 CRC64;

Alignment Scores:
Pred. No.: 2.14e+04 Length: 36
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x IAA STRAU (1-36)

QY 256 GCCTCTCGGCCCCC 242
DB 3 GlycerProAlaPro 7

RESULT 26
MPG2_DACGL STANDARD; PRT; 36 AA.
AC 041183; |||||
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Pollen allergen Dac g 2 (Dac g II) (Fragment).
OS Dactylis glomerata (Orchard grass) (Cockfoot grass).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OC Poaceae; Dactylis.
OX NCBI_Taxid=4509;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=92406239; PubMed=1526648;
RA Roberts A.M., van Ree R., Cardy S.M., Bevan L.J., Walker M.R.;
RT "Recombinant pollen allergens from Dactylis glomerata: preliminary
RT evidence that human IgE cross-reactivity between Dac g II and Lol p
RT I/II is increased following grass pollen immunotherapy.";
RL Immunology 76:389-396(1992).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- ALLERGEN: Causes an allergic reaction in human. Causes grass
CC pollen allergy. Binds IgE.
CC -1- SIMILARITY: Belongs to the expansin family.

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CC or send an email to license@isb-sib.ch).

DR EMBL: S45354; AAB23303.1; ALT_TERM.
DR HSSP: P43214; IMHO.
DR InterPro: IPR007117; Expan_Lol_pI_C.
DR Pfam: PF01357; Pollen_allergen_1.
DR ProDom: PD002179; Expan_Lol_pI_C; 1.
KW Allergen.
FT NON TER 1 1
FT NON TER 36 36
SQ SEQUENCE 36 AA; 3971 MW; B7FFB416DD0E0852 CRC64;

Alignment Scores:
Pred. No.: 2.14e+04 Length: 36
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x MPG2_DACGL (1-36)

QY 276 GAGGTAGAACTCAAG 262


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Db      32 GluValGluLeuIys 36
|||||
RESULT 27
PY MYOSC STANDARD; PRT; 36 AA.
ID PY MYOSC
AC P09641;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Peptide Y1-like (PY1).
OS Myoxocephalus scorpius (Shorthorn sculpin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthopterygii; Acanthopterygii; Percomorpha; Scorpaeniformes;
OC Cottoidei; Cottidae; Myoxocephalus.
NC NCB1_TaxID=8097;
RX TISSUE=Pancreas;
RX MEDLINE=87190954; PubMed=2883025;
RA Cutfield S.M., Carne A., Cutfield J.F.;
RT "The amino-acid sequences of sculpin islet somatostatin-28 and
RL Peptide Y1."
RL FEBS Lett. 214:57-61 (1987).
RN [2]
RP SEQUENCE.
RX MEDLINE=87176585; PubMed=3562898;
RA Conlon J.M., Schmidt W.B., Gallwitz B., Palmer S., Thim L.;
RT "Characterization of an amidated form of pancreatic polypeptide from
RL the daddy sculpin (Cottus scorpius).";
RL Regul. Pept. 16:261-268 (1986).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the NPY family.
DR PIR; A60309; YFPTS.
DR HSSP; P01303; IROK.
DR InterPro; IPR001955; Pancreatic_hormn.
DR Pfam; PF00159; hormone3.1.
DR PRINTS; PR00278; PANCHORMONE.
DR PRODOM; PD001267; Pancreatic_hormn; 1.
DR SMART; SM00309; PAH; 1.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE; PS50276; PANCREATIC_HORMONE_2; 1.
KW Hormone; Amidation.
FT MOD RES 36 AMIDATION.
SQ SEQUENCE 36 AA; 4170 MW; 16F331B73643D7AA CRC64;

Alignment Scores:
Pred. No.: 2.14e+04 Length: 36
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.78% Indels: 0
Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x PY MYOSC (1-36)
QY 79 CCAGGGGCGATGCT 93
DB 8 ProGlyGlyAsnAla 12
|||||
RESULT 28
FL3A_BOVIN STANDARD; PRT; 37 AA.
ID FL3A_BOVIN
AC P12260;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Gamma-glutamyltransferase A chain (BC 2.3.2.13) (Protein-glutamine
DE gamma-glutamyltransferase A chain) (Transglutaminase A chain)
DE (Fragment).
FL3A1 OR FL3A.
GN Bos taurus (Bovine).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
NC NCB1_TaxID=9913;
RN [1]
RP SEQUENCE.
RX MEDLINE=74172215; PubMed=4831071;
RA Nakamura S., Iwanaga S., Suzuki T., Mikuni Y., Konishi K.;
RT "Amino acid sequence of the peptide released from bovine factor XIII
RL following activation by thrombin."
RL Biochem. Biophys. Res. Commun. 58:250-256 (1974).
CC -1- FUNCTION: Factor XIII is activated by thrombin and calcium ion to
CC a transglutaminase that catalyzes the formation of gamma-glutamyl-
CC epsilon-lysine cross-links between fibrin chains, thus stabilizing
CC the fibrin clot. Also cross-link alpha-2-plasmin inhibitor, or
CC fibrinectin, to the alpha chains of fibrin.
CC -1- CATALYTIC ACTIVITY: Protein glutamine + alkylamine = protein N(5)-
CC alkylglutamine + NH(3).
CC -1- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -1- SUBUNIT: Tetramer of two A chains and two B chains.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic in most tissues, but also
CC secreted in the blood plasma.
CC -1- PTM: The activation peptide is released by thrombin.
CC -1- SIMILARITY: Belongs to the transglutaminase family.
DR PIR; A10933; A10933.
DR HSSP; P04488; IGGY.
DR InterPro; IPR001102; GlutransfG.
DR PROSITE; PS00547; TRANSGLUTAMINASES; PARTIAL.
KW Transferase; Acyltransferase; Plasma; Acetylation; Blood coagulation;
KW Calcium-binding; Zymogen.
FT PROPEP 1 37
FT MOD RES 1 1 ACETYLATION PEPTIDE.
FT NON_TER 37 37 ACETYLATION (BY SIMILARITY).
SQ SEQUENCE 37 AA; 3795 MW; 95700493889638CB CRC64;

Alignment Scores:
Pred. No.: 2.14e+04 Length: 37
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.78% Indels: 0
Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x FL3A_BOVIN (1-37)
QY 242 GGGGGCGGAGAGCC 256
DB 9 GlyGlyArgArgAla 13
|||||
RESULT 29
PSBY_CYACA STANDARD; PRT; 37 AA.
ID PSBY_CYACA
AC O19893;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Photosystem II protein Y.
DE PSBY OR YCF32 OR YCF8.
GN Cyanidium caldarium.
OS Cyanidium caldarium.
OC Chloroplast.
OC Eukaryota; Rhodophyta; Bangiophyceae; Porphyridiales; Porphyridiaceae;
OC Cyanidium.
NC NCB1_TaxID=2771;
RN [1]
RP SEQUENCE FROM N.A.
RP STRAIN=RK-1;
RX MEDLINE=20496959; PubMed=11040290;
RA Gloeckner G., Rosenthal A., Valentin K.-U.;
RT "The structure and gene repertoire of an ancient red algal plastid
RL genome."
RL J. Mol. Evol. 51:382-390 (2000).
CC -1- FUNCTION: Manganese-binding polypeptide with L-arginine
CC metabolizing enzyme activity. Component of the core of photosystem

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CC II (By similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane.
CC -1- SIMILARITY: Belongs to the psbJ family.

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CC EMBL: AF022186; AAB82696.1; -
DR PIR: T11961; T11961.
DR HAMAP: MF 00717; -; 1.
KW Photosynthesis; Photosystem II; Transmembrane; Thylakoid; Chloroplast.
FT DOMAIN 1 4 LUMENAL (POTENTIAL).
FT TRANSMEM 5 23 POTENTIAL.
FT DOMAIN 24 37 STROMAL (POTENTIAL).
SQ SEQUENCE 37 AA; 4135 MW; CB79E52D798C35B1 CRC64;

Alignment Scores:
Pred. No.: 2.14e+04 Length: 37
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x PSBY_CVACA (1-37)
QY 60 GGCTCTGTGGCCATC 46
Db 16 Alasertripalatte 20

RESULT 30
SCKA_TITTDI STANDARD; PRT; 37 AA.
AC PS9925;
ID 15-MAR-2004 (Rel. 43, Created)
DT 15-MAR-2004 (Rel. 43, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Toxin Tk1 (Alpha-KTx 4.3).
OS Tityus discrepans (Venezuelan scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butioidae; Butidae; Tityus.
OX NCBI_TaxID=57059;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Venom;
RX MEDLINE=99379616; PubMed=10452547;
RA D'Suze G., Zamudio F., Gomez-Lagunas F., Possani L.D.;
RT "A novel K+ channel blocking toxin from Tityus discrepans scorpion
RT venom".
RU FEBS Lett. 456:146-148 (1999).
CC -1- FUNCTION: Blocks reversibly Shaker B potassium-channels.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- MASS SPECTROMETRY: MW=3816.8; METHOD=MALDI.
CC -1- SIMILARITY: Belongs to the short scorpion toxin family. Potassium
CC channel inhibitor subfamily.
DR PROSITE: PS01138; SCORP_SHORT_TOXIN; 1.
KW Toxin; Ionic channel inhibitor; Neurotoxin;
FT DISULFID 7 28 Potassium channel inhibitor.
FT DISULFID 13 33 BY SIMILARITY.
FT DISULFID 17 33 BY SIMILARITY.
FT SITE 26 33 INTERACTION WITH CA(2+)-ACTIVATED K(+) CHANNELS (POTENTIAL).
SQ SEQUENCE 37 AA; 3826 MW; 6DC2FA311C38542P CRC64;

Alignment Scores:
Pred. No.: 2.14e+04 Length: 37

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x SKKA_TITTDI (1-37)
QY 472 GCGAAGCTGCTGGA 458
Db 22 GlyysaAaAagly 26

RESULT 31
SCKA_TITSE STANDARD; PRT; 37 AA.
AC P4614;
ID 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Tityustoxin K alpha (TSK4) (Alpha-KTx4.1).
DE Tityus serrulatus (Brazilian scorpion).
OS Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones;
OC Butioidae; Butidae; Tityus.
OX NCBI_TaxID=6887;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94151352; PubMed=7509073;
RA Rogowski R.S., Krueger B.K., Collins J.H., Blaustein M.P.;
RT "Tityustoxin K alpha blocks voltage-gated noninactivating K+ channels
RT and unblocks inactivating K+ channels blocked by alpha-dendrotoxin in
RT synaptosomes".
RT Proc. Natl. Acad. Sci. U.S.A. 91:1475-1479 (1994).
RN [2]
RN ERRATUM.
RP Rogowski R.S., Krueger B.K., Collins J.H., Blaustein M.P.;
RA Proc. Natl. Acad. Sci. U.S.A. 93:12051-12051 (1996).
CC -1- FUNCTION: Blocks voltage-gated non-inactivating potassium channels
CC and unblocks inactivating potassium channels blocked by alpha-
CC dendrotoxin in synaptosomes. Binds to a site on the inactivating
CC potassium channel that does not occlude the pore. Its binding
CC apparently prevents alpha-DTX, but not charybotoxin, from
CC blocking the pore.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Belongs to the short scorpion toxin family. Potassium
CC channel inhibitor subfamily.
DR PDB: 1HP2; 1JUN-01.
DR InterPro: IPR001947; Scorpion_toxins.
DR Pfam: PF00451; toxin_2; 1.
DR ProDom: PD003586; Scorpion_toxins; 1.
DR PROSITE: PS01138; SCORP_SHORT_TOXIN; 1.
KW Toxin; Neurotoxin; Ionic channel inhibitor;
KW Potassium channel inhibitor; 3D-structure.
FT DISULFID 7 28 BY SIMILARITY.
FT DISULFID 13 33 BY SIMILARITY.
FT DISULFID 17 35 BY SIMILARITY.
FT SITE 26 33 INTERACTION WITH CA(2+)-ACTIVATED K(+) CHANNELS (POTENTIAL).
SQ SEQUENCE 37 AA; 3948 MW; 639B98A977335929 CRC64;

Alignment Scores:
Pred. No.: 2.14e+04 Length: 37
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x SKKA_TITSE (1-37)
QY 472 GCGAAGCTGCTGGA 458
|||||

Db 22 GlyLyAlaAlaGly 26

RESULT 32

CU47_LACCU STANDARD; PRT; 38 AA.

AC P80323;

DT 01-OCT-1994 (Rel. 30, Created)

DT 01-OCT-1994 (Rel. 30, Last sequence update)

DT 01-FEB-1995 (Rel. 31, Last annotation update)

DE Bacteriocin curvaticin FS47 (Fragment).

OS Lactobacillus curvatus.

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;

OC Lactobacillus.

OX NCBI_TaxID=28038;

RN [1]

RP SEQUENCE.

RC STRAIN=FS47;

RX MEDLINE=94304185; PubMed=8031103;

RA Garver K.I., Muriana P.M.;

RT "Purification and partial amino acid sequence of curvaticin FS47, a heat-stable bacteriocin produced by *Lactobacillus curvatus* FS47.";

RL Appl. Environ. Microbiol. 60:2191-2195(1994).

CC -1- FUNCTION: BACTERIOCIN ACTIVE AGAINST *LISTERIA MONOCYTOGENES*, *PEDIOCOCCUS*, *ENTEROCOCCUS*, *LACTOBACILLI* AND *BACILLI*.

CC -1- SUBCELLULAR LOCATION: Secreted.

DR InterPro: IPR000437; Prok_lipoprot_S.

KW Antibiotic; Bacteriocin.

FT UNSURE 6 6

FT UNSURE 13 13

FT UNSURE 35 36

FT UNSURE 38 38

FT NON TER 38 38

SQ SEQUENCE 38 AA; 3429 MW; 94C354FDFD28BF83 CRC64;

Alignment Scores:

Pred. No.: 2.13e+04 Length: 38

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.78% Indels: 0

DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x CU47_LACCU (1-38)

Oy 139 GCGCGAGGCGAGCA 153

Db 19 GlyAlaGlyAlaAla 23

RESULT 33

EXEL_HELSTU STANDARD; PRT; 38 AA.

ID EXEL_HELSTU

AC P04203;

DT 20-MAR-1987 (Rel. 04, Created)

DT 20-MAR-1987 (Rel. 04, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Exendin-1 (Helopectins I and II).

OS Heloderma suspectum (Gila monster).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidodactylus; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;

OC Heloderma.

OX NCBI_TaxID=8554;

RN [1]

RP SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=85006896; PubMed=6207171;

RA Parker D.S., Rautman J.-P., O'Donohue T.L., Bledsoe M., Yoshida H.,

RA Piasano J.J.;

RT "Amino acid sequences of helopectins, new members of the glucagon superfamily, found in *Gila monster* venom.";

RL J. Biol. Chem. 259:11751-11755(1984).

CC -1- FUNCTION: Has a VIP/secretin-like biological activity.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -1- SIMILARITY: Belongs to the glucagon family.

DR InterPro: IPR000532; Glucagon.

DR Pfam: PF00123; hormone2; 1.

DR SMART: SM00070; GLUCA; 1.

DR PROSITE: PS00260; GLUCAGON; 1.

KW Glucagon family; toxin.

FT VARIANT 38 38

SQ SEQUENCE 38 AA; 4096 MW; 54275BCFC368314A CRC64;

Alignment Scores:

Pred. No.: 2.13e+04 Length: 38

Score: 5.00 Matches: 5

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 2.78% Indels: 0

DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x EXEL_HELSTU (1-38)

Oy 266 AGTCTACCTCGGCA 280

Db 29 SerSerThrSerPro 33

RESULT 34

RR12_PINCO STANDARD; PRT; 38 AA.

ID RR12_PINCO

AC P49168;

DT 01-FEB-1996 (Rel. 33, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Chloroplast 30S ribosomal protein S12 (Fragment).

GN RPS12.

OS Pinus contorta (Shore pine) (Lodgepole pine).

OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.

OX NCBI_TaxID=3339;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Needle;

RX MEDLINE=9503026; PubMed=7999999;

RA Clarke A.K., Gustafsson P., Lidholm J.A.;

RT "Identification and expression of the chloroplast c1p2 gene in the conifer *Pinus contorta*."

RL Plant Mol. Biol. 26:851-862(1994).

CC -1- FUNCTION: With S4 and S5 plays an important role in translational accuracy. Located at the interface of the 30S and 50S subunits (By similarity).

CC -1- SUBUNIT: Part of the 30S ribosomal subunit.

CC -1- SUBCELLULAR LOCATION: Chloroplast.

CC -1- SIMILARITY: Belongs to the S12P family of ribosomal proteins.

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CC -----

DR EMBL: L28807; AAA68095.1; -.

DR PIR: S50764; S50764.

DR HAMAP: MF_00403; 1.

DR InterPro: IPR008994; Nucleic_acid-OB.

DR InterPro: IPR006032; Ribosomal_S12_23.

DR Pfam: PF00164; Ribosomal_S12; 1.

DR PROSITE: PS00055; RIBOSOMAL_S12; PARTIAL.

KW Ribosomal protein; rRNA-binding; rRNA-binding; Chloroplast.

FT NON TER 38 38

SQ SEQUENCE 38 AA; 4406 MW; F7B84D004067D85C CRC64;

Alignment Scores:

Pred. No.: 2.13e+04 Length: 38

Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x RR12_PINCO (1-38)

OY 75 ATCAGGAATGCCAGG 61
DB 8 IleaYgAsMAlaYg 12

RESULT 35

EXE3_HELHO STANDARD; PRT; 39 AA.

ID EXE3_HELHO STANDARD; PRT; 39 AA.
AC P20394;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Exendin-3.
OS Heloderma horridum horridum (Mexican beaded lizard).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidodactylus; Squamata; Scleroglossa; Anguimorpha; Helodermatidae;
OC Heloderma.
NCBI_TaxID=8552;
OK NCB1_TaxID=8552;
RN NCB1_TaxID=8552;
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=91056067; PubMed=1700785;
RA Eng J., Andrew P.C., Kleinman W.A., Singh L., Raufman J.-P.,
RT "Purification and structure of exendin-3, a new pancreatic
RL secretagogue isolated from Heloderma horridum venom."
RL J. Biol. Chem. 265:20259-20262(1990).
CC -1- FUNCTION: Has a VIP/secretin-like biological activity. Interacts
CC with the exendin receptor.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Belongs to the glucagon family.
DR PIR: A23674; HMGH3Z.
DR HSRP: P01275; 1BH0.
DR InterPro: IPR000532; Glucagon.
DR Pfam: PF00123; hormone2; 1.
DR SMART: SM00070; GLUCA; 1.
DR PROSITE: PS00260; GLUCAGON; 1.
KW Glucagon family; Toxin; Amidation.
FT MOD RES 39 AMIDATION.
FT MOD RES 39

SO SEQUENCE 39 AA; 4204 MW; AA4251D3A4B1D1B9 CRC64;

Alignment Scores:

Pred. No.: 2.12e+04 Length: 39
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x EXE3_HELHO (1-39)

OY 182 GGGGCGCCCTCCGCC 168

DB 34 GtYAlaPProProPro 38

RESULT 36

ID MSDB_DROME STANDARD; PRT; 40 AA.

AC O9VBL7: Q24391;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Accessory gland-specific peptide 57db precursor (Male accessory gland
DE secretory protein 57db).
GN M5757DB OR CG5016.
OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OK NCB1_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A., TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RC STRAIN=Oregon-R; TISSUE=Male accessory gland;
RX MEDLINE=95227188; PubMed=7711745;
RA Stimmer E., Schaefer M., Schaefer U.,
RT "Structure and regulation of a gene cluster for male accessory gland
RT transcripts in Drosophila melanogaster."
RL Insect Biochem. Mol. Biol. 25:127-137(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Berkley;
RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.C., Champé M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Gholdek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D.A., Heiman T.J., Hernandez J.R., Houck J.,
RA Hoston D., Houston K.A., Howland T.J., Wei M.-H., Ibbegan C.,
RA Itaili M., Kalush F., Karpen G.H., Ke Z., Kemnison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J.H., Li Z., Liang Y., Lin X.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusser D.R., Paclet J.M.,
RA Palazolo M., Plittman G.S., Pan S., Pollard V., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spadling A.C., Stapleton M., Strong R., Sun B.,
RA Svrtkaskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster."
RL Science 287:2185-2195(2000).
CC -1- FUNCTION: Transferred from male to female during mating and may
CC affect egg-laying and behavior after mating.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Lumen fluid of male accessory glands, becomes
CC seminal fluid.
CC -1- DEVELOPMENTAL STAGE: Last day of pupal development and adults.
CC -----
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CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL: Z33647; CAA83926.1; -
DR EMBL: AE003753; AAF56514.1; -
DR FlyBase: FBgn0011669; M5757DB.
KW Signal; Behavior.

```
FT SIGNAL 1 17 POTENTIAL.
FT CHAIN 18 40 ACCESSORY GLAND-SPECIFIC PEPTIDE 57DB.
FT CONFLICT 37 37 S -> N (IN REF. 1).
SQ SEQUENCE 40 AA; 4184 MW; 66F14C76C2649B50 CRC64;

Alignment Scores:
Pred. No.: 2.12e+04 Length: 40
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x MSDS_DROME (1-40)

QY 488 GTGATCCACATCAAC 474
DB 30 Vailletshilean 34

RESULT 37
Y041_TREPA STANDARD; PRT; 40 AA.
AC 083082;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DN Hypothetical protein TP0041.
OS Treponema pallidum.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Treponema.
OX NCBI_TaxID=160;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nichols;
RX MEDLINE=98332770; PubMed=9665876;
RA Fraiser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwin M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardson J.M., McLeod P.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Uterback T.,
RA McDonald L., Ariach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Harch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete."
CC Science 281:375-388(1998).
-----
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-----
CC EMBL: AE001189; AAC65041.1; -
DR PIR: H71373; H71373.
DR TIGR: TP0041; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 40 AA; 4391 MW; EEDB3D96FEECB9B4 CRC64;

Alignment Scores:
Pred. No.: 2.12e+04 Length: 40
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Y041_TREPA (1-40)

QY 116 GCACCCGCTCTCTCT 102
DB 14 AlaprolaserPro 18
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RESULT 38
RLA2_WHEAT STANDARD; PRT; 42 AA.
ID RLA2_WHEAT
AC P05350;
DT 01-NOV-1988 (Rel. 09, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE 60S acidic ribosomal protein P2 (Ribosomal protein 'A') (Fragment).
OS Triticum aestivum (Wheat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Triticeae; Triticum.
OX NCBI_TaxID=4565;
RN [1]
RP SEQUENCE.
RC TISSUE=Germ;
RX MEDLINE=80001353; PubMed=476516;
RA Vincent L.P., Yaguchi M., Matheson A.T.;
RT "Structural homologues in alanine-rich acidic ribosomal proteins from
RT procarvones and eucaryotes."
RL Can. J. Biochem. 57:719-726(1979).
CC -1- FUNCTION: Plays an important role in the elongation step of
CC protein synthesis.
CC -1- SUBUNIT: P1 and P2 exist as dimers at the large ribosomal subunit.
CC -1- PM: Phosphorylated (By similarity).
CC -1- SIMILARITY: Belongs to the L12P family of ribosomal proteins.
DR PIR: S00295; S00295.
KW Ribosomal protein; Phosphorylation.
FT VARIANT 3 3
FT NON TER 42 42 L -> F.
SQ SEQUENCE 42 AA; 4411 MW; 81D6869AFA14745F CRC64;

Alignment Scores:
Pred. No.: 2.1e+04 Length: 42
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.78% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x RLA2_WHEAT (1-42)

QY 437 AGCTCTCCATCAGCT 451
DB 16 SerserProserala 20

RESULT 39
COA2_XANCP STANDARD; PRT; 43 AA.
ID COA2_XANCP
AC Q07482;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative minor coat protein (ORF43)
DN (GVIT-1 OR XCC2060) AND (GVIT-2 OR XCC2073).
OS Xanthomonas campestris (pv. campestris), and
OS Xanthomonas campestris; Gammaproteobacteria; Xanthomonadales;
OC Bacteriota; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340; 28365;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=X.c.campestris; STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=2202145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach P.C., Farah C.S., Furian L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Canavan F., Cardoso J., Chambergo F., Cláudia L.P.,
RA Cicarelli R.M.B., Coutinho L.V., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
```

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sana J.A.D., Silva C., de Souza R.F.,
RA Spínola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezsa R.I.D.,
RA Teubal J.C., Kiteajima J.P., Truffi D., Tsai S.M., White F.F.,
RA "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities."
RL Nature 417:459-463(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Phage phi-Lf;
RX MEDLINE=94157455; PubMed=8113723;
RA Wen F.-S., Tseng Y.-H.;
RT "Nucleotide sequence determination, characterization and purification
of the single-stranded DNA-binding protein and major coat protein of
filamentous phage phi-Lf of Xanthomonas campestris pv. campestris."
RL J. Gen. Virol. 75:115-22(1994).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL, AE012313; AM41349.1; -;
DR EMBL, AE012313; AM41362.1; -;
DR EMBL, X70331; CAA49797.1; -;
DR PIR, S33483; S33483.
KW Coat protein; Complete proteome.
SQ SEQUENCE 43 AA; 4683 MW; 693EF8AE4FBE6F3 CRC64;

Alignment Scores:
Pred. No.: 2.1e+04 Length: 43
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x COA2_XANCP (1-43)

OY 39 GCGCGTCGACCCCC 25
DB 39 AIAAAGATGThPro 43

RESULT 40
CPC6 CANPG STANDARD; PRT; 43 AA.
AC P81585;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Cuticle protein CP434 (CPCP434).
OS Cancer pagurus (Rock crab).
OC Eukaryota, Metazoa, Arthropoda, Crustacea, Malacostraca;
OC Eumalacostraca, Eucarida, Decapoda, Pleocyemata, Brachyura;
OC Eubrachyura, Cancroidea, Cancridae, Cancer.
OX NCBI_TaxID=6755;
RN [1]
RP SEQUENCE.
RC TISSUE=carapace cuticle;
RX MEDLINE=99354472; PubMed=10425740;
RA Andersen S.O.;
RT "Exoskeletal proteins from the crab, Cancer pagurus."
RL Comp. Biochem. Physiol. 123A:203-211(1999).
CC -1- TISSUE SPECIFICITY: Calcified shell.
CC -1- MASS SPECTROMETRY: MW=4337.2; METHOD=Plasma desorption.
KW Structural protein; Cuticle; Repeat.
FT REPEAT 1
FT REPEAT 18

FT REPEAT 25 42 2.
SQ SEQUENCE 43 AA; 4338 MW; 3AFC471E067D9832 CRC64;
Alignment Scores:
Pred. No.: 2.1e+04 Length: 43
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x CPC6_CANPG (1-43)

OY 80 GGGCCATCGAGATG 66
DB 4 GlyProSerGlyMet 8

RESULT 41
LCCC_LEUME
ID LCCC_LEUME STANDARD; PRT; 43 AA.
AC P81053;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Bacteriocin leucocin C.
OS Leuconostoc mesenteroides.
OC Bacteria; Firmicutes; Lactobacillales; Leuconostoc.
OX NCBI_TaxID=1245;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=2212295; PubMed=12127968;
RA Finland G., Sletten K., Nissen-Meyer J.;
RT "The complete amino acid sequence of the pediocin-like antimicrobial
peptide leucocin C."
RL Biochem. Biophys. Res. Commun. 295:826-827(2002).
RN [2]
RP SEQUENCE OF 1-36.
RC STRAIN=TA33a;
RX MEDLINE=98274743; PubMed=9611809;
RA Papatheasopoulos M.A., Dykes G.A., Revol-Junelles A.-M., Delfour A.,
RA von Holy A., Hastings J.W.;
RT "Sequence and structural relationships of leucocins A-, B- and
C-TA33a from Leuconostoc mesenteroides TA33a."
RL Microbiology 144:1343-1348(1998).
CC -1- FUNCTION: Inhibits a wide spectrum of lactic acid bacteria.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MASS SPECTROMETRY: MW=4595; METHOD=MALDI.
CC -1- SIMILARITY: BELONGS TO THE BACTERIOCIN CLASS IIA/YGNV FAMILY.
CC HSP; P34034; 2LEU.
DR InterPro: IPR002633; Bacteriocin_II.
DR Pfam: PF01721; Bacteriocin_II; 1.
DR ProDom: PD004452; Bacteriocin_II; 1.
KW Antibiotic; Bacteriocin.
FT DISULFD 9 14
FT CONFLICT 22 22 BY SIMILARITY.
FT W->A (IN REF. 2).
SQ SEQUENCE 43 AA; 4598 MW; 926382483FBE65C3 CRC64;

Alignment Scores:
Pred. No.: 2.1e+04 Length: 43
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.78% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x LCCC_LEUME (1-43)

OY 82 GGGGCGATGCTGCG 96
DB 36 GlyGlyMetAlaGly 40

RESULT 42
NLTP_RAPSA

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ID NLTP_RAPSA STANDARD; PRT; 43 AA.
AC P29420;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DE Seed nonspecific lipid transfer protein-like (LTP) (Fragment).
OS Raphanus sativus (Raphan).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucosids II; Brassicales; Brassicaceae; Raphanus.
CX NCBI_TaxID=3726;
RN [1]
RP SEQUENCE.
RC Tissue=Seed;
RA Terras F.R.G., Gederis I.J., van Leuven F., Vanderleyden J.,
RA Cammue B.P.A., Broekaert W.F.,
"in vitro antifungal activity of a radish (Raphanus sativus L.) seed
protein homologous to non-specific lipid transfer proteins.";
RT Plant Physiol. 100:1055-1058(1992).
RL -1- FUNCTION: Plant nonspecific lipid-transfer proteins transfer
phospholipids as well as galactolipids across membranes. May play
a role in wax or cutin deposition in the cell walls of expanding
epidermal cells and certain secretory tissues. This isoform
inhibits the hyphal growth of several fungi in vitro.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: Belongs to the plant LTP family.
DR HSSP; P19656; IMEM.
DR InterPro; IPR003612; AAT.
DR InterPro; IPR00528; PLANT_LTP.
DR Pfam; PF00234; tryp_alpha_aml1. 1.
DR PRINTS; PR00382; LIPIDTRANSFER.
DR PROSITE; PS00597; PLANT_LTP; PARTIAL.
KW Plant defense; Lipid-binding; Transport; Fungicide.
FT NON TER 43
SQ SEQUENCE 43 AA; 4311 MW; A723ABE610EDDCAF CRC64;

Alignment Scores:
Pred. No.: 2.1e+04 Length: 43
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x NLTP_RAPSA (1-43)
QY 364 GCACCCCTGCGACG 350
DB 22 AlaproteolalArg 26

RESULT 43
PSBY_SYNPK STANDARD; PRT; 43 AA.
AC PS59908;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Photosystem II protein Y.
OS PSBY OR SYN0898.
OC Synecchococcus sp. (strain WH8102).
OC Bacteria; Cyanobacteria; Chroococcales; Synecchococcus.
CX NCBI_TaxID=84588;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=22825697; PubMed=12917641;
RA Patenk B., Brahmsha B., Larimer F.W., Land M., Hauser L., Chain P.,
RA Lamerdin B., Regala W., Allen E.E., McCarren J., Paulsen I.,
RA Dufresne A., Patensky F., Webb E.A., Waterbury J.;
"the genome of a motile marine Synecchococcus.";
RT Nature 424:1037-1042(2003).
RL -1- FUNCTION: Manganese-binding polypeptide with L-arginine
metabolizing enzyme activity. Component of the core of photosystem
II (By similarity).

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CC -1- SUBCELLULAR LOCATION: Cellular thylakoid membrane.
CC -1- SIMILARITY: Belongs to the psby family.
CC -----
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CC -----
DR EMBL; BX569691; CAB07413.1; -
DR HAMAP; MF_00717; -; 1.
KW Photosynthesis; Photosystem II; Transmembrane; Thylakoid;
KW Complete proteome.
FT TRANSMEM 8
SQ SEQUENCE 43 AA; 4592 MW; B84DB86A0A3F1DA CRC64;

Alignment Scores:
Pred. No.: 2.1e+04 Length: 43
Score: 5.00 Matches: 5
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 2.81% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x PSBY_SYNPK (1-43)
QY 442 AGACCTGCGAGTTGCG 428
DB 28 ArgalaalValGly 32

RESULT 44
SBOA_BACSU STANDARD; PRT; 43 AA.
AC 007623;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Subtilisin A precursor (Antibacterial bacteriocin subtilisin).
OS SBOA OR SBO OR BSU37350.
OC Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
CX NCBI_TaxID=1423;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 6633 / LH45;
RA Stein T., Duesterhus S., Entian K.D.;
"Subtilisin A biosynthesis is conserved among two different classes of
RT Bacillus subtilis strains.";
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98015417; PubMed=935933;
RA Prescian E., Moszer I., Boursier L., Cruz Ramos H.C., De la Fuente V.,
RA Hullo M.-F., Lejong C., Schleich S., Sekowska A., Song B.H.,
RA Villani G., Kunst F., Danchin A., Glaser P.;
"the Bacillus subtilis genome from gerBC (311 degrees) to 11cR (334
RT degrees)";
RL Microbiology 143:3313-3328(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Besieres P., Bolotin A., Borchert S.,
RA Borries R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Bruller S., Brunsch C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Duesterhoft A., Ehrlich S.D., Emmerison P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galazzi A., Galleron N.,

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RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
 RA Guilepeli G., Guy B.J., Haga K., Halech J., Harwood C.R., Hentat A.,
 RA Hilbert H., Holsappel S., Hosono S., Hultio M.F., Iraya M., Jones L.,
 RA Joris B., Karmata D., Kasahara Y., Klaerr-Bianchini M., Klein C.,
 RA Kobayashi Y., Koetter P., Konigstein G., Krogh S., Kumano M.,
 RA Kurita K., Lapidus A., Lardinois S., Luber J., Lazarevic V.,
 RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
 RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
 RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
 RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
 RA Presecan E., Pujic P., Purnelle B., Rapoport G., Ray M., Reynolds S.,
 RA Rieger M., Rivolta E., Roche E., Roche B., Rose M., Sedat Y.,
 RA Sato T., Scanlan E., Schleich S., Schroeter R., Scofield P.,
 RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
 RA Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K.,
 RA Tachuchi M., Tamakoshi A., Tanaka T., Tempira P., Tononi A.,
 RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
 RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
 RA Winters P., Wiput A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
 RA Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.,
 RT "The complete genome sequence of the Gram-positive bacterium *Bacillus*
 RT *subtilis*":
 RT Nature 390:249-256(1997).
 RL Nature 390:249-256(1997).
 RN [4]
 RN SEQUENCE OF 9-43, CHARACTERIZATION, AND MASS SPECTROMETRY.
 RP STRAIN=168;
 RX MEDLINE=8611663; PubMed=3936839;
 RA Babasak K., Takao T., Shimomishi Y., Kurahashi K.;
 RT "Subtilisin A, a new antibiotic peptide produced by *Bacillus subtilis*
 RT 168: isolation, structural analysis, and biogenesis.";
 RL J. Biochem. 98:585-603(1985).
 RN [5]
 RN FUNCTION.
 RP STRAIN=168 / JH642, and 22a;
 RX MEDLINE=20042357; PubMed=10572140;
 RA Zheng G., Yan L.Z., Vederas J.C., Zuber P.;
 RT "Genes of the *sbo*-*alb* locus of *Bacillus subtilis* are required for
 RT production of the antilisterial bacteriocin subtilisin.";
 RL J. Bacteriol. 181:7346-7355(1999).
 RN [6]
 RN TRANSCRIPTIONAL REGULATION.
 RP STRAIN=168 / JH642;
 RX MEDLINE=20270160; PubMed=10809710;
 RA Nakano M.M., Zheng G., Zuber P.;
 RT "Dual control of *sbo*-*alb* operon expression by the *Spoo* and *Reed*
 RT systems of signal transduction under anaerobic conditions in *Bacillus*
 RT *subtilis*.";
 RL J. Bacteriol. 182:3274-3277(2000).
 RN [7]
 RN STRUCTURE BY NMR, AND CYS-PHE AND CYS-THR INTRACHAIN CROSS-LINKS.
 RP MEDLINE=22583854; PubMed=1256888;
 RA Kawilka K., Sprules T., McKay R.T., Mercier P., Diaper C.M., Zuber P.,
 RA Vederas J.C.;
 RT "Structure of subtilisin A, an antimicrobial peptide from *Bacillus*
 RT *subtilis* with unusual posttranslational modifications linking
 RT cysteine sulfurs to alpha-carbons of phenylalanine and threonine.";
 RL J. Am. Chem. Soc. 125:4726-4727(2003).
 RN [8]
 RN STEREOCHEMISTRY OF D-ALLO-THR-36.
 RP Vederas J.C.;
 RL Unpublished observations (May-2003).
 CC -1- FUNCTION: Has bacteriocidal activity against some Gram-positive
 CC bacteria such as *Listeria*, some species of *Bacillus* and *E.faciun*.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- DEVELOPMENTAL STAGE: The production of subtilisin A begins at the
 CC end of vegetative growth and finishes before spore formation.
 CC -1- INDUCTION: Transcription is highly induced by oxygen limitation
 CC and is under dual and independent control of *spo0A*-*abrB* and *resD*.
 CC -1- PTM: This peptide undergoes unique processing steps that include
 CC proteolytic cleavage after Glu-8, and covalent linkage of the
 CC alpha-amino of Asn-9 with the carboxyl of Gly-43 to form a
 CC cyclopeptide. Thioether cross-links are formed between cysteines
 CC and the alpha-carbons of other amino acids, Cys-12 to Phe-39,

CC Cys-15 to Thr-36, and Cys-21 to Phe-30. In forming these cross-
 CC links, Thr-36 and Phe-39 are converted to D-amino-acids.
 CC -1- MASS SPECTROMETRY: Mw=3398.9; METHOD=FM; RANGE=9-43.
 CC -1- CAUTION: Ref.4 sequence does not report residues in positions 30
 CC and 39 probably due to their modification, and reports a cyclic
 CC permutation of the peptide sequence.
 CC -----
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AJ430547; CAD23198.1; -;
 DR EMBL; Z97024; CAB09701.1; -;
 DR EMBL; Z99123; CAB15763.1; -;
 DR PIR; A69704; A69704.
 DR Subtilisin; Bg12671; sboA.
 KW Antibiotic; Bacteriocin; D-amino acid; Thioether bond;
 KM Complete proteome.
 FT PROBE 1 8
 FT CHAIN 9 43 SUBTILISIN A.
 FT CROSSLINK 9 43 Cyclopeptide (Asn-Gly).
 FT CROSSLINK 12 39 2-cysteiny-D-phenylalanine (Cys-Phe).
 FT CROSSLINK 15 36 2-cysteiny-D-allo-threonine (Cys-Thr).
 FT CROSSLINK 21 30 2-cysteiny-L-phenylalanine (Cys-Phe).
 SQ SEQUENCE 43 AA; 4325 MW; 055A81DA0D378794 CRC64;
 Alignment Scores:
 Pred. No.: 2.1e+04 Length: 43
 Score: 5.00 Matches: 5
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 2.788 Indels: 0
 Db: 1 Gaps: 0
 US-10-023-182-1_COPY_54_593 (1-540) x SBOA_BACSU (1-43)
 QY 109 GCGGGTGCACGCGC 123
 Db 33 AAGIYALATNrgly 37
 RESULT 45
 COAB BPXF STANDARD; PRT; 44 AA.
 AC P03621;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Coat protein B (Major coat protein).
 OS Bacteriophage Xf.
 OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
 ON NCBI_TaxID=10865;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=79086258; PubMed=729805;
 RA Frangione B., Nakashima Y., Konigsberg W., Wiseman R.L.;
 RT "The amino acid sequence of the major coat protein subunit of the
 RT filamentous virus Xf.";
 RL FEBS Lett. 96:381-384(1978).
 RN [2]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=91175634; PubMed=2078529;
 RA Wray D.A.;
 RT "Model-building studies of Inovirus: genetic variations on a
 RT geometric theme.";
 RL Int. J. Biol. Macromol. 12:125-138(1990).
 CC -1- FUNCTION: Coat protein B is the major coat protein of the virion.
 DR PIR; A04230; VCBPXF.
 DR PDB; 2IFO; 30-NOV-94.
 KW Coat protein; Acetylation; 3D-structure.

FT MOD_RSS 1 1 ACETYLATION.
SQ SEQUENCE 44 AA; 4342 MW; ACC9223F5DE63D28 CRC64;

Alignment Scores:

Pred. No.:	2.09e+04	Length:	44
Score:	5.00	Matches:	5
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	2.78%	Indels:	0
DB:	1	Gaps:	0

US-10-023-182-1_COPY_54_593 (1-540) X COAB_BPXF (1-44)

QY	29	GTTCACCGCGCATG	43
Db	40	ValArgArgAlaMet	44

Search completed: July 19, 2004, 12:12:35
Job time : 23 secs

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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 19, 2004, 12:11:51 ; Search time 58 Seconds
(without alignments)
5875.167 Million cell updates/sec

Title: US-10-023-182-1_COPY_54_593
Perfect score: 180
Sequence: 1 ATGCAGGCCGAGAGCCGAGGCGG.....CTCCCTCAGGCGAGAGGCGC 540

Scoring table:
OLIGO
Xgapop 60.0 , Xgapext 60.0
Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1017041 seqs, 315518202 residues

Word size: 1

Total number of hits satisfying chosen parameters: 92578

Minimum DB seq length: 5
Maximum DB seq length: 50

Post-processing: Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p model -DEV=xlp
-Q=/cgn2/1/USPTO_epool/p/US10023182/runatc_19072004_125308_4290/app_query.fasta_1.711
-DB=SPTRMBL_25 -QFMT=faстан -SUFFIX=ol1.rspt -MINMATCH=0.1 -LOOPEL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=ol1igo -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR SCORE=quality -THR MIN=1 -ALIGN=45 -MODE=LOCAL
-OUTMT=ptco -NORM=ext -HEAPSIZE=500 -MINLEN=5 -MAXLEN=50
-USER=US10023182 @CGN 1.1 133 @runatc_19072004_125308_4290 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEROVERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -Fgapop=6
-Fgapext=7 -Ygapop=60 -Ygapext=60 -DELOP=6 -DELEXT=7

Database :

SPTRMBL_25.*
1: sp_archaea.*
2: sp_bacteria.*
3: sp_fungi.*
4: sp_human.*
5: sp_invertebrate.*
6: sp_mammal.*
7: sp_mhc.*
8: sp_organelle.*
9: sp_phage.*
10: sp_plant.*
11: sp_rodent.*
12: sp_virus.*
13: sp_vertebrate.*
14: sp_unclassified.*
15: sp_virus.*
16: sp_bacteriopl.*
17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the total score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match Length	DB ID	Description
C 1	8	4.5	43 2 Q9AM68	Q9am68 xanthomonas

C 2	8	4.5	46 16 Q8PDK1	Q8pdk1 xanthomonas
C 3	7	3.9	37 16 Q8FW45	Q8fw45 brucella su
C 4	7	3.9	40 12 Q8OHM4	Q8ohm4 hepatitis c
C 5	7	3.9	41 4 Q8NE80	Q8ne80 homo sapien
C 6	6	3.3	15 4 Q9UE41	Q9ue41 homo sapien
C 7	6	3.4	15 4 Q9UC90	Q9uc90 homo sapien
C 8	6	3.4	16 4 Q9UC88	Q9uc88 homo sapien
C 9	6	3.4	18 4 Q9UE42	Q9ue42 homo sapien
C 10	6	3.3	20 2 Q9R4H8	Q9r4h8 arthrobacte
C 11	6	3.4	23 4 Q9UCJ9	Q9ucj9 homo sapien
C 12	6	3.4	23 10 Q8SAC4	Q8sac4 amblystegiu
C 13	6	3.4	23 10 Q8SAB8	Q8sab8 amblystegiu
C 14	6	3.4	24 10 Q8SAC7	Q8sac7 amblystegiu
C 15	6	3.4	24 10 Q8SAC1	Q8sac1 amblystegiu
C 16	6	3.4	25 10 Q8SAC3	Q8sac3 amblystegiu
C 17	6	3.4	25 10 Q8RV05	Q8rv05 amblystegiu
C 18	6	3.4	25 10 Q8SAC8	Q8sac8 amblystegiu
C 19	6	3.4	25 10 Q8SAC6	Q8sac6 amblystegiu
C 20	6	3.4	26 10 Q8SAD0	Q8sad0 amblystegiu
C 21	6	3.4	26 10 Q8SAD1	Q8sad1 amblystegiu
C 22	6	3.4	26 10 Q8SAD5	Q8sad5 amblystegiu
C 23	6	3.4	26 10 Q8RV97	Q8rv97 amblystegiu
C 24	6	3.4	26 10 Q8SAC5	Q8sac5 amblystegiu
C 25	6	3.4	27 4 Q9UMA6	Q9uma6 homo sapien
C 26	6	3.4	27 10 Q8SAD6	Q8sad6 amblystegiu
C 27	6	3.4	27 10 Q8SAD0	Q8sad0 amblystegiu
C 28	6	3.4	27 10 Q8SAD3	Q8sad3 amblystegiu
C 29	6	3.4	27 10 Q8SAB9	Q8sab9 amblystegiu
C 30	6	3.4	27 10 Q8SAD2	Q8sad2 amblystegiu
C 31	6	3.4	27 10 Q8SAD4	Q8sad4 amblystegiu
C 32	6	3.4	27 10 Q8SAC9	Q8sac9 amblystegiu
C 33	6	3.4	29 6 Q9X575	Q9x575 sus scrofa
C 34	6	3.4	30 16 Q97GC1	Q97gc1 streptococc
C 35	6	3.4	30 16 Q8PDK2	Q8pdk2 xanthomonas
C 36	6	3.4	31 4 Q9Y2A3	Q9y2a3 homo sapien
C 37	6	3.3	32 5 Q9NNW0	Q9nnw0 plasmodium
C 38	6	3.3	33 12 Q9LJ09	Q9lj09 tt virus
C 39	6	3.3	33 12 Q9LJ08	Q9lj08 tt virus
C 40	6	3.3	34 6 Q9BDF0	Q9bdf0 oryctolagus
C 41	6	3.4	34 16 Q8K58	Q8k58 chlorobium
C 42	6	3.4	36 4 Q9Y2A1	Q9y2a1 homo sapien
C 43	6	3.4	36 16 Q9KN23	Q9kn23 vibrio chol
C 44	6	3.4	37 16 Q7UY29	Q7uy29 rhodospirell
C 45	6	3.3	37 16 Q7UV27	Q7uv27 rhodospirell

ALIGNMENTS

RESULT 1

ID	Q9AM68	PRELIMINARY:	PRT:	43 AA.
AC	Q9AM68			
DT	01-JUN-2001 (TRENBLUREL_17, Created)			
DT	01-JUN-2001 (TRENBLUREL_17, Last sequence update)			
DT	01-MAR-2003 (TRENBLUREL_23, Last annotation update)			
DE	Xanthomonadin biosynthesis related protein 1.			
CN	PICB			
OS	Xanthomonas oryzae (pv. oryzae).			
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;			
OC	Xanthomonadaceae; Xanthomonas.			
OX	NCBI_TaxID=64187;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Zou H., Zhang X., Wang J.			
RT	"Three Novel Pig genes of Xanthomonas oryzae pv. oryzae."			
RL	Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AF329698; AAC50284.1;			
SQ	SEQUENCE 43 AA; 4521 MW; 18E33E3875004FC9 CRC64;			

Alignment Scores:
Pred. No.: 117
Score: 8.00
Percent Similarity: 100.00%

Length: 43
Matches: 8
Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.49% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q9AM68 (1-43)

QY 95 CCAGCATGCCCCCTGGGCGCATCA 72
DB 7 ProAlaLeuProProGlyProSer 14

RESULT 2

Q8PDK1 PRELIMINARY; PRT; 46 AA.

AC Q8PDK1; 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Xanthomonadin biosynthesis related protein 1.
GN XCC0334.

OS Xanthomonas campestris (pv. campestris).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;

OC Xanthomonadaceae; Xanthomonas.

OX NCBI_TaxID=340;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=ATCC 33913 / NCPPB 528;

RA MEDLINE=20224145; PubMed12024217;

RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,

RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,

RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,

RA Camarotte G., Camavan F., Cardoso J., Chamergo F., Clapina L.P.,

RA Ciccarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,

RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,

RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,

RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,

RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,

RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.T., Moon D.H.,

RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,

RA Pereira H.A., Rossi A., Sana J.A.D., Silva C., de Souza R.F.,

RA Spindola L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,

RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,

RA Setubal J.C., Kitzajima J.P.;

RT "Comparison of the genomes of two Xanthomonas pathogens with differing

RT host specificities."

RT host specificities."

RT Nature 417:459-463 (2002).

RL EMBL; AE012129; AAM39653.1; -.

DR EMBL; AE012129; AAM39653.1; -.

OC Complete proteome.

SO SEQUENCE 46 AA; 4540 MW; 55551F0DB7458F95 CRC64;

Alignment Scores:

Pred. No.: 116 Length: 46
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.49% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8PDK1 (1-46)

QY 95 CCAGCATGCCCCCTGGGCGCATCA 72
DB 7 ProAlaLeuProProGlyProSer 14

RESULT 3

Q8FW45 PRELIMINARY; PRT; 37 AA.

AC Q8FW45; 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE Hypothetical protein.

GN BR0620.

OS Brucella suis.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;

OC Brucellaceae; Brucella.

OX NCBI_TaxID=29461;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=1330 / Biovar 1;

RA MEDLINE=22247741; PubMed=12271122;

RA Paulsen I.T., Seeshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,

RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beaman M.J.,

RA Daugherty S.C., Debey R.T., Durkin A.S., Kolonay J.F., Madupu R.,

RA Nelson W.C., Ayodeji B., Krahl M., Shetty J., Malek J., Van Aken S.E.,

RA Hoover D.L., Lindler L.E., Hailing S.W., Boyle S.M., Fraser C.M.,

RA "The Brucella suis genome reveals fundamental similarities between

RT animal and plant pathogens and symbionts."

RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153 (2002).

DR EMBL; AE014558; AAN33809.1; -.

DR TIGR; BR0620; -.

KW Hypothetical protein; Complete proteome.

SO SEQUENCE 37 AA; 3906 MW; BEBCC27948610244 CRC64;

Alignment Scores:

Pred. No.: 1.17e+03 Length: 37
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.93% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8FW45 (1-37)

QY 422 TCTGACGAGTCAGTCGATG 402
DB 18 SerAlaValSerArgile 24

RESULT 4

Q80HH4 PRELIMINARY; PRT; 40 AA.

AC Q80HH4; 01-JUN-2003 (TREMBLrel. 24, Created)

DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

DE 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Polyprotein (Fragment).

OS Hepatitis C virus.

OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;

OC Hepacivirus.

OX NCBI_TaxID=11103;

RN [1] SEQUENCE FROM N.A.

RC STRAIN=1360DD;

RA Keenan E.D., Rousler S.D., Sherman K.E.,

RA "Complexity and diversity of HCV RNA in African Americans,"

RA Submitted (DRC-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY194693; AAO87906.1; -.

KW Polyprotein.

FT NON_TER 1

FT NON_TER 40

SO SEQUENCE 40 AA; 4008 MW; 741182536B1C7598 CRC64;

Alignment Scores:

Pred. No.: 1.16e+03 Length: 40
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.93% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q80HH4 (1-40)

QY 410 AGTCGATGTCAGTATGTTG 390
DB 28 SerArgileValSerMetleu 34

```
RESULT 5
Q8NE80 PRELIMINARY; PRT; 41 AA.
ID Q8NE80
AC Q8NE80.
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Strauberg R.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC034424; AA034424.1; -.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 41 AA; 4599 MW; 21D1D26C5F63A624 CRC64;

Alignment Scores:
Pred. No.: 1.15e+03 Length: 41
Score: 7.00 Matches: 7
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.89% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8NE80 (1-41)

QY 515 CTCAGGCTCCTCGAGGAGA 535
DB 16 LeuSerLeuProGlnGlyArg 22

RESULT 6
Q9UE41 PRELIMINARY; PRT; 15 AA.
ID Q9UE41
AC Q9UE41.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Collagen.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89325561; PubMed=2753125;
RA Viikula M.; Pellonen L.;
RT "Structural analyses of the polymorphic area in type II collagen
gene.";
RL FEBS Lett. 250:171-174(1989).
DR EMBL; X16158; CAA34281.1; -.
SQ SEQUENCE 15 AA; 1334 MW; D6DC3824197ABER6 CRC64;

Alignment Scores:
Pred. No.: 1.26e+04 Length: 15
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q9UE41 (1-15)

QY 100 CCAGAGAGCGGGGCGCC 117
DB 3 ProGlyGlnAlaGlyAla 8

RESULT 7
```

```
Q9UC90 PRELIMINARY; PRT; 15 AA.
ID Q9UC90
AC Q9UC90.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE ONCOFETAL-laminin binding COLLAGENALPHA 1(I) chain, of-UB collagen
alpha 1(I) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95169134; PubMed=7864881;
RA Minafra I.P.; Andriolo W.; Basirico L.; Aquino A.; Minafra S.;
RA Boutillon M.M.; van der Rest M.;
RT "Onco-fetal/laminin-binding collagen from colon carcinoma: detection
of new sequences.";
RL Biochem. Biophys. Res. Commun. 207:852-859(1995).
DR GO; GO:0005581; C:collagen; NAS.
DR GO; GO:0005201; F:extracellular matrix structural constituent; NAS.
DR GO; GO:0005515; F:protein binding; NAS.
DR GO; GO:0007155; P:cell adhesion; NAS.
FT NON TER 1
SQ SEQUENCE 15 AA; 1363 MW; 33BD20878D3B1BF2 CRC64;

Alignment Scores:
Pred. No.: 1.26e+04 Length: 15
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q9UC90 (1-15)

QY 65 CCAGGCGCTCCTGGGCGCA 48
DB 4 ProGlyProProGlyPro 9

RESULT 8
Q9UC88 PRELIMINARY; PRT; 16 AA.
ID Q9UC88
AC Q9UC88.
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE ONCOFETAL-laminin binding COLLAGENALPHA 1(I) chain, of-UB collagen
alpha 1(I) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=95169134; PubMed=7864881;
RA Minafra I.P.; Andriolo W.; Basirico L.; Aquino A.; Minafra S.;
RA Boutillon M.M.; van der Rest M.;
RT "Onco-fetal/laminin-binding collagen from colon carcinoma: detection
of new sequences.";
RL Biochem. Biophys. Res. Commun. 207:852-859(1995).
DR GO; GO:0005581; C:collagen; NAS.
DR GO; GO:0005201; F:extracellular matrix structural constituent; NAS.
DR GO; GO:0005515; F:protein binding; NAS.
DR GO; GO:0007155; P:cell adhesion; NAS.
FT NON TER 1
SQ SEQUENCE 16 AA; 1385 MW; F7F93D20B39D3B1B CRC64;

Alignment Scores:
Pred. No.: 1.25e+04 Length: 16
```

Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q9UC88 (1-16)

Qy 65 CCAGGCGCTCTGGGCCA 48
DB 4 ProglyProProGlyPro 9

RESULT 9

ID Q9UC42 PRELIMINARY; PRT; 18 AA.
AC Q9UC42;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Collagen.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=89325561; PubMed=2753125;
RA Wikula M., Peltonen L.;
RT "Structural analyses of the polymorphic area in type II collagen
gene";
RL FEBS Lett. 250:171-174(1989).
DR EMBL; X16158; CAA34280.1; -.
SQ SEQUENCE 18 AA; 1614 MW; 041D6170BD6D3FA5 CRC64;

Alignment Scores:

Pred. No.: 1.23e+04 Length: 18
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q9UC42 (1-18)

Qy 65 CCAGGCGCTCTGGGCCA 48
DB 3 ProglyProProGlyPro 8

RESULT 10

ID Q9R4H8 PRELIMINARY; PRT; 20 AA.
AC Q9R4H8;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE L2 like ribosomal protein (Fragment).
OS Arthrobacter globiformis.
OC Bacteria; Actinobacteriae; Actinobacteridae; Actinomycetales;
OC Micrococciaceae; Micrococcaceae; Arthrobacter.
OX NCBI_TaxID=1665;
RN (1)
RP SEQUENCE.
RX MEDLINE=96014410; PubMed=8520111;
RA Ochiai K., Kawamoto I.;
RT "Two-dimensional gel electrophoresis of ribosomal proteins as a novel
approach to bacterial taxonomy: application to the genus
Arthrobacter.";
RL Biosci. Biotechnol. Biochem. 59:1679-1687(1995).
SQ SEQUENCE 20 AA; 2193 MW; 45F5C7DDBD84F08D CRC64;

Alignment Scores:

Pred. No.: 1.22e+04 Length: 20
Score: 6.00 Matches: 6

Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 2 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q9R4H8 (1-20)

Qy 135 CCAGGCGCGAGGCGGACG 152
DB 10 ProglyArgArgGlySer 15

RESULT 11

ID Q9UCJ9 PRELIMINARY; PRT; 23 AA.
AC Q9UCJ9;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Gelatinase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE.
RX MEDLINE=93125357; PubMed=1480034;
RA Tschesche H., Knauper V., Kramer S., Michaelis J., Oberhoff R.,
RA Reinke H.;
RT "Latent collagenase and gelatinase from human neutrophils and their
activation";
RL Matrix Suppl. 1:245-255(1992).
DR HSP; P08254; ISLM.
DR GO; GO:0005578; C:extracellular matrix; IEA.
DR GO; GO:0004222; F:metalloendopeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR001818; Pept_M10A_M12B.
DR Pfam; PF03933; Peptidase_M10_N; 1.
DR PROSITE; PS00546; CYSTEINE_SWITCH; 1.
SQ SEQUENCE 23 AA; 2595 MW; 3927C18A3D6BA558 CRC64;

Alignment Scores:

Pred. No.: 1.2e+04 Length: 23
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q9UCJ9 (1-23)

Qy 198 GCCATGCGACCGCGCG 181
DB 1 AlameLArgThrProArg 6

RESULT 12

ID Q8SAC4 PRELIMINARY; PRT; 23 AA.
AC Q8SAC4;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE AtbB (Fragment).
OS Amblystegium varium.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBI_TaxID=111436;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=AV8;
RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Reconciled gene trees, molecular evolution, and species relationships
in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF464970; AAL75467.1; -.
FT NON TER 23
SQ SEQUENCE 23 AA; 2528 MW; B7D0A7EF0742232F CRC64;
Alignment Scores:
Pred. No.: 1.2e+04 Length: 23
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 10 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x Q8SAC4 (1-23)
QY 515 GCCAAAAACACGGGCAGA 498
Db 15 AAlaYsaAnThrGlyArg 20
RESULT 13
Q8SAB8 PRELIMINARY; PRT; 23 AA.
ID Q8SAB8
AC Q8SAB8; 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE AtPB (Fragment).
OS Amblystegium noterophilum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBI_TaxID=185235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ANA4;
RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Reconciled gene trees, molecular evolution, and species relationships
in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464976; AAL75473.1; -.
FT NON TER 23
SQ SEQUENCE 23 AA; 2528 MW; B7D0A7EF0742232F CRC64;
Alignment Scores:
Pred. No.: 1.2e+04 Length: 23
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 10 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x Q8SAB8 (1-23)
QY 515 GCCAAAAACACGGGCAGA 498
Db 15 AAlaYsaAnThrGlyArg 20
RESULT 14
Q8SAC7 PRELIMINARY; PRT; 24 AA.
ID Q8SAC7
AC Q8SAC7; 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE AtPB (Fragment).
OS Amblystegium tenax.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBI_TaxID=111435;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AT8;
RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Reconciled gene trees, molecular evolution, and species relationships
in Amblystegium (Bryopsida).";

RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464967; AAL75464.1; -.
FT NON TER 24
SQ SEQUENCE 24 AA; 2691 MW; 4417D0A7EF074223 CRC64;
Alignment Scores:
Pred. No.: 1.2e+04 Length: 24
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 10 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x Q8SAC7 (1-24)
QY 515 GCCAAAAACACGGGCAGA 498
Db 15 AAlaYsaAnThrGlyArg 20
RESULT 15
Q8SAC1 PRELIMINARY; PRT; 24 AA.
ID Q8SAC1
AC Q8SAC1; 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE AtPB (Fragment).
OS Amblystegium noterophilum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBI_TaxID=185235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ANB1;
RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Reconciled gene trees, molecular evolution, and species relationships
in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464973; AAL75470.1; -.
FT NON TER 24
SQ SEQUENCE 24 AA; 2691 MW; 4417D0A7EF074223 CRC64;
Alignment Scores:
Pred. No.: 1.2e+04 Length: 24
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 10 Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x Q8SAC1 (1-24)
QY 515 GCCAAAAACACGGGCAGA 498
Db 15 AAlaYsaAnThrGlyArg 20
RESULT 16
Q8SAC3 PRELIMINARY; PRT; 25 AA.
ID Q8SAC3
AC Q8SAC3; 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE AtPB (Fragment).
OS Amblystegium varium.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBI_TaxID=111436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV9;
RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Reconciled gene trees, molecular evolution, and species relationships

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RT in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464971; AAL75468.1; -.
FT NON TER 25
SQ SEQUENCE 25 AA; 2804 MW; 53D417D0A7EF0742 CRC64;

Alignment Scores:
Pred. No.: 1.19e+04 Length: 25
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 10 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8RV05 (1-25)
QY 515 GCCAAAACACGGCGAGA 498
DB 15 AAlaYsAnThrGlyArg 20

RESULT 17
Q8RV05 PRELIMINARY; PRT; 25 AA.
ID Q8RV05;
AC Q8RV05;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE AltpB (Fragment).
OS Amblystegium humile.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBI_TaxID=111433;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AH3a, and AH3;
RT "Reconciled gene trees, molecular evolution, and species relationships
RT in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464960; AAL75457.1; -.
FT NON TER 25
SQ SEQUENCE 25 AA; 2754 MW; 54BF17D0A7EF0742 CRC64;

Alignment Scores:
Pred. No.: 1.19e+04 Length: 25
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 10 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8RV05 (1-25)
QY 515 GCCAAAACACGGCGAGA 498
DB 15 AAlaYsAnThrGlyArg 20

RESULT 18
Q8SAC8 PRELIMINARY; PRT; 25 AA.
ID Q8SAC8;
AC Q8SAC8;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE AltpB (Fragment).
OS Amblystegium tenax.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBI_TaxID=111435;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RT7;
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RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Reconciled gene trees, molecular evolution, and species relationships
RT in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464966; AAL75463.1; -.
FT NON TER 25
SQ SEQUENCE 25 AA; 2754 MW; 53CF17D0A7EF0742 CRC64;

Alignment Scores:
Pred. No.: 1.19e+04 Length: 25
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 10 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8SAC8 (1-25)
QY 515 GCCAAAACACGGCGAGA 498
DB 15 AAlaYsAnThrGlyArg 20

RESULT 19
Q8SAC6 PRELIMINARY; PRT; 25 AA.
ID Q8SAC6;
AC Q8SAC6;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE AltpB (Fragment).
OS Amblystegium tenax.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBI_TaxID=111435;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AT9;
RT "Reconciled gene trees, molecular evolution, and species relationships
RT in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464968; AAL75465.1; -.
FT NON TER 25
SQ SEQUENCE 25 AA; 2754 MW; 54BF17D0A7EF0742 CRC64;

Alignment Scores:
Pred. No.: 1.19e+04 Length: 25
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 10 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8SAC6 (1-25)
QY 515 GCCAAAACACGGCGAGA 498
DB 15 AAlaYsAnThrGlyArg 20

RESULT 20
Q8SAD0 PRELIMINARY; PRT; 26 AA.
ID Q8SAD0;
AC Q8SAD0;
DT 01-JUN-2002 (TREMBlrel. 21, Created)
DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
DE AltpB (Fragment).
OS Amblystegium humile.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBI_TaxID=111433;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=AH5;
RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Reconciled gene trees, molecular evolution, and species relationships
RT in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464962; AAL75459.1; -.
FT NON TER 26
SQ SEQUENCE 26 AA; 2811 MW; 0724BF17D0A7EF07 CRC64;

Alignment Scores:
Pred. No.: 1.19e+04 Length: 26
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8SAD0 (1-26)
OY 515 GCCAAACACGGCGCAGA 498
DB 15 AlalysaenthrglyArg 20

RESULT 21
Q8SAD1 PRELIMINARY; PRT; 26 AA.
ID Q8SAD1;
AC Q8SAD1;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE AtPB (Fragment).
OS Amblystegium humile.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBI_TaxID=11433;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AH4;
RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Reconciled gene trees, molecular evolution, and species relationships
RT in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464961; AAL75458.1; -.
FT NON TER 26
SQ SEQUENCE 26 AA; 2861 MW; 0723D417D0A7EF07 CRC64;

Alignment Scores:
Pred. No.: 1.19e+04 Length: 26
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8SAD1 (1-26)
OY 515 GCCAAACACGGCGCAGA 498
DB 15 AlalysaenthrglyArg 20

RESULT 22
Q8SAD5 PRELIMINARY; PRT; 26 AA.
ID Q8SAD5;
AC Q8SAD5;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE AtPB (Fragment).
OS Amblystegium fluviale.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBI_TaxID=140014;
RN [1]
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RP SEQUENCE FROM N.A.
RC STRAIN=AF3;
RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Reconciled gene trees, molecular evolution, and species relationships
RT in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464955; AAL75452.1; -.
FT NON TER 26
SQ SEQUENCE 26 AA; 2934 MW; 07378417D0A7EF07 CRC64;

Alignment Scores:
Pred. No.: 1.19e+04 Length: 26
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8SAD5 (1-26)
OY 515 GCCAAACACGGCGCAGA 498
DB 15 AlalysaenthrglyArg 20

RESULT 23
Q8RV97 PRELIMINARY; PRT; 26 AA.
ID Q8RV97;
AC Q8RV97;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE AtPB (Fragment).
OS Amblystegium serpens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBI_TaxID=99400;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ASA;
RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Reconciled gene trees, molecular evolution, and species relationships
RT in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464963; AAL75460.1; -.
FT NON TER 26
SQ SEQUENCE 26 AA; 2976 MW; 1D878417D0A7EF07 CRC64;

Alignment Scores:
Pred. No.: 1.19e+04 Length: 26
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8RV97 (1-26)
OY 515 GCCAAACACGGCGCAGA 498
DB 15 AlalysaenthrglyArg 20

RESULT 24
Q8SAC5 PRELIMINARY; PRT; 26 AA.
ID Q8SAC5;
AC Q8SAC5;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE AtPB (Fragment).
OS Amblystegium varium.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
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OX NCB1_TaxID=111436;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AV2;
RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Reconciled gene trees, molecular evolution, and species relationships
in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464969; AAL75466.1; -.
FT NON TER
SQ SEQUENCE 26 AA; 2811 MW; 0724BF17D0A7EF07 CRC64;

Alignment Scores:
Pred. No.: 1.18e+04
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 3.37%
DB: 10

US-10-023-182-1_COPY_54_593 (1-540) x Q8SAD6 (1-26)

QY 515 GCCAATAACACGGGCGAGA 498
DB 15 AAlaYsAsnThrGlyArg 20

RESULT 25
Q8UMA6 PRELIMINARY; PRT; 27 AA.
ID Q9UMA6;
AC Q9UMA6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Type I collagen alpha 1 chain (Fragment).
GN COL1A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93237886; PubMed=8097422;
RA Cohn D.H., Zhang X., Byers P.H.;
RT "Homology-mediated recombination between type I collagen gene exons
RT results in an internal tandem duplication and lethal osteogenesis
RT imperfecta.";
RL Hum. Mutat. 2:21-27(1993).
DR EMBL; S58915; AAB26324.1; -.
DR InterPro; IPR008160; Collagen.
KW Collagen.
FT NON TER
SQ SEQUENCE 27 AA; 2496 MW; E9BCD23967CEABCD CRC64;

Alignment Scores:
Pred. No.: 1.18e+04
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 3.37%
DB: 4

US-10-023-182-1_COPY_54_593 (1-540) x Q9UMA6 (1-27)

QY 65 CCAGGGCTTCCTGGGCCA 48
DB 21 ProGlyProProGlyPro 26

RESULT 26
Q8SAD6 PRELIMINARY; PRT; 27 AA.
ID Q8SAD6;
AC Q8SAD6;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
PT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
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DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AtPB (Fragment).
OS Amblystegium fluviatile.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCB1_TaxID=140014;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AP2;
RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Reconciled gene trees, molecular evolution, and species relationships
in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464954; AAL75451.1; -.
FT NON TER
SQ SEQUENCE 27 AA; 2898 MW; 71C724BF17D0A7EF CRC64;

Alignment Scores:
Pred. No.: 1.18e+04
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 3.37%
DB: 10

US-10-023-182-1_COPY_54_593 (1-540) x Q8SAD6 (1-27)

QY 515 GCCAATAACACGGGCGAGA 498
DB 15 AAlaYsAsnThrGlyArg 20

RESULT 27
Q8SAC0 PRELIMINARY; PRT; 27 AA.
ID Q8SAC0;
AC Q8SAC0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AtPB (Fragment).
OS Amblystegium noterophilum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCB1_TaxID=185235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ANA2;
RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Reconciled gene trees, molecular evolution, and species relationships
in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464974; AAL75471.1; -.
FT NON TER
SQ SEQUENCE 27 AA; 2908 MW; 731723CF17D0A7EF CRC64;

Alignment Scores:
Pred. No.: 1.18e+04
Score: 6.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 3.37%
DB: 10

US-10-023-182-1_COPY_54_593 (1-540) x Q8SAC0 (1-27)

QY 515 GCCAATAACACGGGCGAGA 498
DB 15 AAlaYsAsnThrGlyArg 20

RESULT 28
Q8SAD3 PRELIMINARY; PRT; 27 AA.
ID Q8SAD3;
AC Q8SAD3;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
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DT 01-JUN-2002 (TReMBLrel. 21, last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE AcpB (Fragment)
OS Amblystegium sepiens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBJ_TaxID=99400;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Aha;
RA "Reconstructed gene trees, molecular evolution, and species relationships
RT in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464957; AAL75454.1; -.
FT NON TER 27
SQ SEQUENCE 27 AA; 2880 MW; 71C724BF1BE0A7EF CRC64;

Alignment Scores:
Pred. No.: 1.18e+04 Length: 27
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8SAB9 (1-27)
OY 515 GCCAATAACACGGCGACGA 498
DB 15 AAlayasanthrighlyarg 20
|||||
|||||

RESULT 29
Q8SAB9 PRELIMINARY; PRT; 27 AA.
ID Q8SAB9
AC Q8SAB9;
DT 01-JUN-2002 (TReMBLrel. 21, Created)
DT 01-JUN-2002 (TReMBLrel. 21, last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, last annotation update)
DE AcpB (Fragment).
OS Amblystegium noterophilum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBJ_TaxID=185235;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ANA3;
RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Reconstructed gene trees, molecular evolution, and species relationships
RT in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464975; AAL75472.1; -.
FT NON TER 27
SQ SEQUENCE 27 AA; 3090 MW; 707737841D70A7EF CRC64;

Alignment Scores:
Pred. No.: 1.18e+04 Length: 27
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8SAB9 (1-27)
OY 515 GCCAATAACACGGCGACGA 498
DB 15 AAlayasanthrighlyarg 20
|||||
|||||

RESULT 30
Q8SAD2 PRELIMINARY; PRT; 27 AA.
ID Q8SAD2
AC Q8SAD2;

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DT	01-JUN-2002 (T-EMBLrel. 21, Created)	
DT	01-JUN-2002 (T-EMBLrel. 21, Last sequence update)	
DT	01-JUN-2002 (T-EMBLrel. 21, Last annotation update)	
DE	AtPB (Fragment). 1	
OS	Amblystegium humile.	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;	
OC	Bryophida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.	
OX	NCBI_TaxID=111433;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=AHaa;	
RA	Vanderpoorten A., Shaw A.J., Cox C.J.;	
RT	"Reconciled gene trees, molecular evolution, and species relationships	
RT	in Amblystegium (Bryopsida)."	
RL	Submitted (JAN-2002) to the EMBL/genbank/DBJ databases.	
DR	EMBL; AF464958; AAL75455.1; -.	
FT	NON TER	27
SQ	SEQUENCE	27 AA; 2884 MW; 73173E15ABE0A7BF CRC64;
Alignment Scores:		
Pred. No.:	1.18e+04	Length: 27
Score:	6.00	Matches: 6
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	3.37%	Indels: 0
DB:	10	Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x Q8SAD2 (1-27)		
QY	515 GCCAAAACACGGCGCAGA 498	
DB	15 AlalysasanthrclYarg 20	
RESULT 31		
ID	Q8SAD4	PRELIMINARY; PRT; 27 AA.
AC	Q8SAD4;	
DT	01-JUN-2002 (T-EMBLrel. 21, Created)	
DT	01-JUN-2002 (T-EMBLrel. 21, Last sequence update)	
DT	01-JUN-2002 (T-EMBLrel. 21, Last annotation update)	
DE	AtPB (Fragment).	
OS	Amblystegium fluviatile.	
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;	
OC	Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.	
OX	NCBI_TaxID=140014;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=AF10;	
RA	Vanderpoorten A., Shaw A.J., Cox C.J.;	
RT	"Reconciled gene trees, molecular evolution, and species relationships	
RT	in Amblystegium (Bryopsida)."	
RL	Submitted (JAN-2002) to the EMBL/genbank/DBJ databases.	
DR	EMBL; AF464956; AAL75453.1; -.	
FT	NON TER	27
SQ	SEQUENCE	27 AA; 2901 MW; 6C0873CC652B9BAF CRC64;
Alignment Scores:		
Pred. No.:	1.18e+04	Length: 27
Score:	6.00	Matches: 6
Percent Similarity:	100.00%	Conservative: 0
Best Local Similarity:	100.00%	Mismatches: 0
Query Match:	3.37%	Indels: 0
DB:	10	Gaps: 0
US-10-023-182-1_COPY_54_593 (1-540) x Q8SAD4 (1-27)		
QY	515 GCCAAAACACGGCGCAGA 498	
DB	15 AlalysasanthrclYarg 20	
RESULT 32		
ID	Q8SAC9	PRELIMINARY; PRT; 27 AA.

```
AC Q8SAC9;
DC 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AtgB (Fragment).
OS Amblystegium tenax.
OC Bryopsida; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Bryopsida; Bryidae; Hypnales; Amblystegiaceae; Amblystegium.
OX NCBI_TaxId=111435;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AT4;
RA Vanderpoorten A., Shaw A.J., Cox C.J.;
RT "Reconciled gene trees, molecular evolution, and species relationships
in Amblystegium (Bryopsida).";
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF464965; AAL75462.1; -.
FT NON_TER 27 27
SQ SEQUENCE 27 AA; 2898 MW; 71C724BF17DDA7EF CRC64;

Alignment Scores:
Pred. No.: 1.18e+04 Length: 27
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8SAC9 (1-27)

QY 515 GCCAAAACACGGCGACA 498
DB 15 AAlayASanThrglyArg 20

RESULT 33
Q9XS75 PRELIMINARY; PRT; 29 AA.
ID Q9XS75;
DC 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE Uncoupling protein 1 (Fragment).
OS UCPL.
OS Sus scrofa domestica (domestic pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9825;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=9269917; PubMed=10337623;
RA Larsen N.J., Marklund S., Kelly K.A., Malek M., Tuggle C.K., Yerle M.,
RA Rothschild M.F.;
RT "New insights into porcine-human synteny conservation.";
RL Mamm. Genome 10:488-491(1999).
DR EMBL; AF060561; AAD26529.1; -.
FT NON_TER 1 1
SQ SEQUENCE 29 AA; 3346 MW; CA21789334C1D4DE CRC64;

Alignment Scores:
Pred. No.: 1.18e+04 Length: 29
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q9XS75 (1-29)

QY 455 CAGAGCTGATGAGAGGC 438
DB 16 GIngluLeuMetG1user 21

RESULT 34
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Q970G1
ID Q970G1 PRELIMINARY; PRT; 30 AA.
AC Q970G1;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE Hypothetical protein SP1253.
GN SP1253.
OS Streptococcus pneumoniae.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxId=1313;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC BAA-334 / TIGR4;
RX MEDLINE=21357209; PubMed=11463916;
RA Teterlin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
RA Peterson S., Heidelberg J., Deboy R.T., Haft D.H., Dodson R.J.,
RA Durkin A.S., Gwinn W., Kolonay J.F., Nelson W.C., Peterson J.D.,
RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Rådune D.,
RA Holtzapple E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L.,
RA McDonald L.A., Feldlyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
RT "Complete genome sequence of a virulent isolate of Streptococcus
pneumoniae.";
RL Science 293:498-506(2001).
DR EMBL; AE007425; AAK75358.1; -.
DR PIR; E95145; E95145.
DR TIGR; SP1253; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 30 AA; 3347 MW; 7BD1AAEA37D5979 CRC64;

Alignment Scores:
Pred. No.: 1.17e+04 Length: 30
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q970G1 (1-30)

QY 314 GCCAGCTGCTTCATG 297
DB 14 A1aserSerA1aserMet 19

RESULT 35
Q8PDK2 PRELIMINARY; PRT; 30 AA.
ID Q8PDK2;
DC 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Xanthomonadin biosynthesis related protein 1.
GN XCC0332.
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxId=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Parah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.B.A.,
RA Camarotte G., Camarvan F., Cardoso J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.M., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locati E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
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RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinoia L.A.F., Takita M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities";
RL Nature 417:459-463(2002).
DR EMBL: AE012129; AAM39652.1; -.
KW Complete proteome.
SQ SEQUENCE 30 AA; 3080 MW; BC2AA8BBA368384 CRC64;

Alignment Scores:
Pred. No.: 1.17e+04 Length: 30
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8PDK2 (1-30)
QY 95 CCAGCATTGCCCTGGG 78
DB 7 ProalaleuPrologly 12

RESULT 36
QY9Y2A3 PRELIMINARY; PRT; 31 AA.
AC Q9Y2A3;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE P53TGI-D.
GN P53TGI.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98377792; PubMed=97113990;
RA Takei Y., Ishikawa S., Tokino T., Muto T., Nakamura Y.;
RT "Isolation of a novel TP53 target gene from a colon-cancer cell line
carrying a highly regulated wild-type TP53 expression system";
RL Genes Chromosomes Cancer 23:1-9(1998).
DR EMBL: AB007458; BAA78643.1; -.
DR GO: GO:0005634; C:nucleus; NAS.
DR GO: GO:0006974; P:response to DNA damage stimulus; NAS.
SQ SEQUENCE 31 AA; 3415 MW; CB7C54537B958D5A CRC64;

Alignment Scores:
Pred. No.: 1.17e+04 Length: 31
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q9Y2A3 (1-31)
QY 261 CAGGCGGCTTCGGGCC 244
DB 18 GlnAlaLeuArgPro 23

RESULT 37
Q9NNW0 PRELIMINARY; PRT; 32 AA.
AC Q9NNW0;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Hypothetical protein (Fragment).
OS Plasmidium falciparum (isolate 3D7).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmidium.
OX NCBI_TaxID=36329;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3D7;
RX MEDLINE=2103610; PubMed=11163452;
RA Spielmann T., Beck H.P.;
RT "Analysis of stage-specific transcription in Plasmidium falciparum
RT reveals a set of genes exclusively transcribed in ring stage
RT parasites.";
RL Mol. Biochem. Parasitol. 111:453-458 (2000).
DR EMBL: AJ290920; CAB92929.2; -.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 32
SQ SEQUENCE 32 AA; 3735 MW; A3CC7BC0A5625B8A CRC64;

Alignment Scores:
Pred. No.: 1.16e+04 Length: 32
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q9NNW0 (1-32)
QY 47 ATGGCCGAGAGGCCCTG 64
DB 8 Metahinginglialaleu 13

RESULT 38
Q91J09 PRELIMINARY; PRT; 33 AA.
AC Q91J09;
DT 01-DEC-2001 (TReMBLrel. 19, Created)
DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE ORF2 (Fragment).
OS TT virus.
OC Viruses; ssDNA viruses; Circoviridae; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=mother-5;
RA Lin H.-H., Kao J.-H., Lee P.-I., Chen D.-S.;
RT "Early acquisition of TT virus in infants: Probable minor role of
RT maternal transmission";
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF380381; AAK59295.1; -.
FT NON_TER 1
FT NON_TER 33
SQ SEQUENCE 33 AA; 3759 MW; 36A10E18A5ED3037 CRC64;

Alignment Scores:
Pred. No.: 1.16e+04 Length: 33
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q91J09 (1-33)
QY 198 CGGCGGCTTCAGGCT 215
DB 18 ArgArgGlyPheArgAla 23

RESULT 39
Q91J08 PRELIMINARY; PRT; 33 AA.
ID Q91J08

```
AC Q91J08;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE ORF2 (Fragment).
OS TT virus.
OC Viruses; ssDNA viruses; Circoviridae; Anellovirus.
OX NCBI_TaxID=68887;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=baby-5;
RA Lin H.-H., Kao J.-H., Lee P.-I., Chen D.-S.;
RT "Early acquisition of TT virus in infants: Probable minor role of
  maternal transmission.";
RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF380382; AAK59296.1; -.
FT NON_TER 1 33
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3731 MW; 36BD6268AE5D3037 CRC64;

Alignment Scores:
Pred. No.: 1.16e+04 Length: 33
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 12 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q91J08 (1-33)
QY 198 CGCGCGGCTTCAGGCT 215
Db 18 ArgArgGlyPheArgAla 23

RESULT 40
Q9BDF0 PRELIMINARY; PRT; 34 AA.
AC Q9BDF0;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE UORF.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21369883; PubMed=11328811;
RA Moroni A., Gorza L., Belltrame M., Gravante B., Vaccari T.,
RA Bianchi M.E., Altomare C., Longhi R., Heurteaux C., Vltadello M.,
RA Malgaroli A., DiFrancesco D.;
RT "Hyperpolarization-activated Cyclic Nucleotide-gated Channel 1 Is a
  RT Molecular Determinant of the Cardiac Pacemaker Current If.";
RL J. Biol. Chem. 276:28233-29411(2001).
DR EMBL; AF168122; AAK19916.1; -.
SQ SEQUENCE 34 AA; 3874 MW; 1B8752522DC04DAB CRC64;

Alignment Scores:
Pred. No.: 1.16e+04 Length: 34
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 6 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q9BDF0 (1-34)
QY 233 GCGGCGCCAGCGGCGG 250
Db 29 AlaGlyProGlyGlyArg 34

RESULT 41
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Q8KB58
ID Q8KB58 PRELIMINARY; PRT; 34 AA.
AC Q8KB58;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hypothetical protein CT1933.
OS Chlorobium tepidum.
OC Bacteria; Chlorobi; Chlorobia; Chlorobiales; Chlorobiaceae;
OC Chlorobium.
OX NCBI_TaxID=1097;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TL5 / ATCC 49652 / DSM 12025;
RX MEDLINE=22103685; PubMed=12093901;
RA Eisen J.A., Nelson K.E., Paulsen I.T., Heidelberg J.F., Wu M.,
RA Dodson R.U., Debey R., Gwinn M.L., Nelson W.C., Haft D.H.,
RA Hickey E.R., Peterson J.D., Durkin A.S., Kolonay J.L., Yang F.,
RA Holt I., Umayam L.A., Mason T., Brenner M., Shea T.P., Parksey D.,
RA Niernan W.C., Feldblyum T.V., Hansen C.L., Craven M.B., Radune D.,
RA Vamthavan J., Khouri H., White O., Gruber T.M., Ketchum K.A.,
RA Venter J.C., Telcelin H., Bryant D.A., Fraser C.M.;
RT "The complete genome sequence of Chlorobium tepidum TL5, a
  RT photosynthetic, anaerobic, green-sulfur bacterium.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:9509-9514(2002).
DR EMBL; AE012944; AAM73152.1; -.
DR TIGR; CT1933; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 34 AA; 4119 MW; 3154F50F0B208606 CRC64;

Alignment Scores:
Pred. No.: 1.16e+04 Length: 34
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 16 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q8KB58 (1-34)
QY 295 GTGTGCGAAGGCGATGG 278
Db 8 ValSerArgLysAlaIrrp 13

RESULT 42
Q9Y2A1 PRELIMINARY; PRT; 36 AA.
ID Q9Y2A1;
AC Q9Y2A1;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE P53ng1-B.
GN P53ng1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98377792; PubMed=9713990;
RA Takai Y., Ishikawa S., Tokino T., Muto T., Nakamura Y.;
RT "Isolation of a novel TP53 target gene from a colon-cancer cell line
  RT carrying a highly regulated wild-type TP53 expression system.";
RL Genes Chromosomes Cancer 23:1-9(1998).
DR EMBL; AB007456; BA478641.1; -.
DR GO; GO:0005634; C:nucleus; NAS.
DR GO; GO:0006974; P:response to DNA damage stimulus; NAS.
SQ SEQUENCE 36 AA; 3827 MW; F3445854FE2185C5 CRC64;

Alignment Scores:
Pred. No.: 1.15e+04 Length: 36
Score: 6.00 Matches: 6
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 4 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q9Y2A1 (1-36)
QY 261 GAGCGGCTCTCCGCGCC 244
Db 18 GluAlaIaIeAArgPro 23

RESULT 43
Q9KN23 PRELIMINARY; PRT; 36 AA.
ID Q9KN23;
AC Q9KN23;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Hypothetical protein VCA0143.
GN VCA0143.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwin M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Baes S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Uterback T., Fleischmann R.D., Nieman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae."
RL Nature 406:477-483(2000).
DR EMBL; AB004355; AAP6056.1; -
DR PIR; A82496; A82496.
DR TIGR; VCA0143; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 36 AA; 4357 MW; C9AC4A9380AB7724 CRC64;

Alignment Scores:
Pred. No.: 1.15e+04 Length: 36
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 16 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q9KN23 (1-36)
QY 517 GAGCGAAACACGCGCA 500
Db 8 GluProIystrAArgAla 13

RESULT 44
Q7UY29 PRELIMINARY; PRT; 37 AA.
ID Q7UY29;
AC Q7UY29;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN RB922.
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
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RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294134; CAD71819.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 37 AA; 3999 MW; 3A25C2F67B20BC17 CRC64;

Alignment Scores:
Pred. No.: 1.15e+04 Length: 37
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.37% Indels: 0
DB: 16 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q7UY29 (1-37)
QY 429 GCGGTGCTGCGACGACT 412
Db 11 AlaValAlaCysSerSer 16

RESULT 45
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ID Q7UVZ7;
AC Q7UVZ7;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein.
GN RB2350.
OS Rhodospirillum rubrum.
OC Bacteria; Planctomycetes; Planctomycetacia; Planctomycetales;
OC Planctomycetaceae; Pirellula.
OX NCBI_TaxID=117;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1;
RX MEDLINE=22735913; PubMed=12835416;
RA Gloeckner F.O., Kube M., Bauer M., Teeling H., Lombardot T.,
RA Ludwig W., Gade D., Beck A., Borzym K., Heilmann K., Rabus R.,
RA Schlesner H., Amann R., Reinhardt R.;
RT "Complete genome sequence of the marine planctomycete Pirellula sp.
RT strain 1."
RL Proc. Natl. Acad. Sci. U.S.A. 100:8298-8303(2003).
DR EMBL; BX294137; CAD72574.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 37 AA; 4199 MW; BBD62AEAD5C23D6 CRC64;

Alignment Scores:
Pred. No.: 1.15e+04 Length: 37
Score: 6.00 Matches: 6
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.33% Indels: 0
DB: 16 Gaps: 0

US-10-023-182-1_COPY_54_593 (1-540) x Q7UVZ7 (1-37)
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Db 28 GluLeuAlaArgArgSer 33

Search completed: July 19, 2004, 12:15:28
Job time : 60 secs
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GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: July 21, 2004, 11:02:28 ; Search time 0.001 Seconds
(without alignments)
894.240 Million cell updates/sec

Title: US-10-023-182-1

Perfect score: 180
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 82 segs, 828 residues

Total number of hits satisfying chosen parameters: 164

Minimum DB seq length: 5
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 82 summaries

Command line parameters:
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-DB=ra1.pep -SUFFIX=ptc -OUT=davis182-1.ra1 -MINMATCH=0.1 -LOOPL=0
-TROOPS=0 -UNITS=bits -START=54 -END=593 -MATRIX=unitary_AA
-TRANS=human40.cdi -LIST=82 -DOALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=82 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=5
-MAXLEN=50 -NCPU=6 -NO_XIPXY -NEG_SCORES=0 -LONGIOG -THREADS=1 -XGAPOP=10
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Database : ra1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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5	18	10.0	18	1	US-09-359-503-12
6	18	10.0	18	1	US-09-359-503-13
7	18	10.0	18	1	US-09-183-931-42
8	11	6.1	11	1	US-09-359-503-4
9	11	6.1	11	1	US-09-062-422-4
10	11	6.1	11	1	US-08-937-263B-4
11	11	6.1	11	1	US-09-166-448-79
12	11	6.1	11	1	US-09-705-160-42
13	11	6.1	11	1	US-09-440-621-1
14	11	6.1	11	1	US-09-697-884-79
15	11	6.1	11	1	US-09-751-798-4
16	11	6.1	11	1	US-09-344-040C-130
17	11	6.1	11	1	US-09-574-749B-33
18	11	6.1	11	1	US-09-676-005B-1
19	11	6.1	11	1	US-09-833-039A-130
20	10	5.6	10	1	US-09-359-503-7
21	10	5.6	10	1	US-09-344-040C-126

22	10	5.6	10	1	US-09-344-040C-127	Sequence 127, App
23	10	5.6	10	1	US-09-344-040C-128	Sequence 128, App
24	10	5.6	10	1	US-09-344-040C-129	Sequence 129, App
25	10	5.6	10	1	US-09-676-005B-11	Sequence 11, Appl
26	10	5.6	10	1	US-09-833-039A-126	Sequence 126, App
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28	10	5.6	10	1	US-09-833-039A-128	Sequence 128, App
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30	10	5.0	10	1	US-09-183-931-43	Sequence 43, Appl
31	9	5.0	9	1	US-09-183-931-44	Sequence 44, Appl
32	9	5.0	9	1	US-09-359-503-5	Sequence 5, Appl1
33	9	5.0	9	1	US-09-359-503-6	Sequence 6, Appl1
34	9	5.0	9	1	US-09-062-422-5	Sequence 5, Appl1
35	9	5.0	9	1	US-09-062-422-6	Sequence 6, Appl1
36	9	5.0	9	1	US-08-937-263B-5	Sequence 5, Appl1
37	9	5.0	9	1	US-08-937-263B-6	Sequence 6, Appl1
38	9	5.0	9	1	US-09-166-448-80	Sequence 80, Appl
39	9	5.0	9	1	US-09-166-448-81	Sequence 81, Appl
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44	9	5.0	9	1	US-09-697-884-80	Sequence 80, Appl
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48	9	5.0	9	1	US-09-670-456A-3	Sequence 3, Appl1
49	9	5.0	9	1	US-09-751-798-5	Sequence 5, Appl1
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55	9	5.0	9	1	US-09-344-040C-117	Sequence 117, App
56	9	5.0	9	1	US-09-344-040C-118	Sequence 118, App
57	9	5.0	9	1	US-09-344-040C-119	Sequence 119, App
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59	9	5.0	9	1	US-09-344-040C-121	Sequence 121, App
60	9	5.0	9	1	US-09-344-040C-122	Sequence 122, App
61	9	5.0	9	1	US-09-344-040C-123	Sequence 123, App
62	9	5.0	9	1	US-09-344-040C-124	Sequence 124, App
63	9	5.0	9	1	US-09-344-040C-125	Sequence 125, App
64	9	5.0	9	1	US-09-344-040C-131	Sequence 131, App
65	9	5.0	9	1	US-09-344-040C-132	Sequence 132, App
66	9	5.0	9	1	US-08-574-749B-34	Sequence 34, Appl
67	9	5.0	9	1	US-09-574-749B-35	Sequence 35, Appl
68	9	5.0	9	1	US-09-676-005B-3	Sequence 3, Appl1
69	9	5.0	9	1	US-09-676-005B-19	Sequence 19, Appl
70	9	5.0	9	1	US-09-833-039A-116	Sequence 116, App
71	9	5.0	9	1	US-09-833-039A-117	Sequence 117, App
72	9	5.0	9	1	US-09-833-039A-118	Sequence 118, App
73	9	5.0	9	1	US-09-833-039A-119	Sequence 119, App
74	9	5.0	9	1	US-09-833-039A-120	Sequence 120, App
75	9	5.0	9	1	US-09-833-039A-121	Sequence 121, App
76	9	5.0	9	1	US-09-833-039A-122	Sequence 122, App
77	9	5.0	9	1	US-09-833-039A-123	Sequence 123, App
78	9	5.0	9	1	US-09-833-039A-124	Sequence 124, App
79	9	5.0	9	1	US-09-833-039A-125	Sequence 125, App
80	9	5.0	9	1	US-09-833-039A-131	Sequence 131, App

ALIGNMENTS

RESULT 1
US-09-359-503-8
; Sequence 8, Application US/09359503
; Patent No. 6231603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, alexander
; TITLE OF INVENTION: Method for Determining Status of A

;; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
;; NUMBER OF SEQUENCES: 14
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fulbright & Jaworski, L.L.P.
;; STREET: 666 Fifth Avenue
;; CITY: New York City
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: WordPerfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/359,503
;; FILING DATE: July 23, 1999
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/165,546
;; FILING DATE: October 2, 1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/062,422
;; FILING DATE: April 17, 1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/937,263
;; FILING DATE: September 15, 1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/752,182
;; FILING DATE: 03-October-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 6251603man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5466.1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 318-3000
;; TELEFAX: (212) 752-5958
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS: 18 amino acids
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; US-09-359-503-8
;;
Alignment Scores:
Pred. No.: 1.21 Length: 18
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.00% Indels: 0
Gaps: 0
DB: 1
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Db 1 A1a1a1a5ph1s1Ar1g1In1eu1n1eu1s1er1Ie1se1r1e1Cys1Le1u1g1In1eu 18
RESULT 2
US-09-359-503-9
; Sequence 9, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, Alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; to NY-

;; CITY: New York City
;; STATE: New York
;; COUNTRY: USA
;; ZIP: 10103
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
;; COMPUTER: IBM
;; OPERATING SYSTEM: PC-DOS
;; SOFTWARE: WordPerfect
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/359,503
;; FILING DATE: July 23, 1999
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/165,546
;; FILING DATE: October 2, 1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 09/062,422
;; FILING DATE: April 17, 1998
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/937,263
;; FILING DATE: September 15, 1997
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/752,182
;; FILING DATE: 03-October-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Hanson, No. 6251603man D.
;; REGISTRATION NUMBER: 30,946
;; REFERENCE/DOCKET NUMBER: LUD 5466.1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 318-3000
;; TELEFAX: (212) 752-5958
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 18 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; US-09-359-503-9
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Alignment Scores:
Pred. No.: 1.21 Length: 18
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.00% Indels: 0
Gaps: 0
DB: 1
US-10-023-182-1 (1-752) x US-09-359-503-9 (1-18)
QY 414 GTGCTTGAAGAGATTCACTGTGTCGCGCAACATGACTATCGAGTACT 467
Db 1 Val1eu1eu1ys1G1u1ph1e1Th1Val1Ser1C1y1Asn1I1eu1Th1r1I1e1A1g1Leu1Th 18
RESULT 3
US-09-359-503-10
; Sequence 10, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, Alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; to NY-

```
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/09/359,503
  FILING DATE: July 23, 1999
CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 09/165,546
    FILING DATE: October 2, 1998
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 09/062,422
    FILING DATE: April 17, 1998
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/937,263
    FILING DATE: September 15, 1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/752,182
    FILING DATE: 03-October-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: Hanson, No. 6251603man D.
    REGISTRATION NUMBER: 30,946
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (212) 318-3000
      TELEFAX: (212) 752-5958
    INFORMATION FOR SEQ ID NO: 10:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 18 amino acids
        TYPE: amino acid
        TOPOLOGY: linear
US-09-359-503-10

Alignment Scores:
Pred. No.:      1.21      Length:      18
Score:          18.00      Matches:      18
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    10.00%      Indels:      0
DB:             1          Gaps:          0

US-10-023-182-1 (1-752) x US-09-359-503-10 (1-18)

Cy      396 CCGGTCCTCCGCGGCGGCTGCTTGAAGAGTTCAGTGTGTCGCGGAGACATA 449
Db      1  ProLeuProValProGlyValLeuValSGluPheInrValSerGlyA5m1le 18

RESULT 4
US-09-359-503-11
Sequence 11, Application US/09359503
Patent No. 6251603
GENERAL INFORMATION:
  APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
  APPLICANT: Knuth, Alexander
  TITLE OF INVENTION: Method for Determining Status of A
  TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
  TITLE OF INVENTION: a Patient Sample
  NUMBER OF SEQUENCES: 14
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fulbright & Jaworski, L.L.P.
    STREET: 666 Fifth Avenue
    CITY: New York City
    STATE: New York
    COUNTRY: USA
    ZIP: 10103
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
  COMPUTER: IBM
  OPERATING SYSTEM: PC-DOS
  SOFTWARE: WordPerfect
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/359,503
    FILING DATE: July 23, 1999
  CLASSIFICATION:
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 09/165,546
      FILING DATE: October 2, 1998
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 09/062,422
      FILING DATE: July 23, 1999
  to NY-
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CLASSIFICATION:
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 09/165,546
    FILING DATE: October 2, 1998
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 09/062,422
    FILING DATE: April 17, 1998
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: 08/937,263
    FILING DATE: September 15, 1997
  PRIOR APPLICATION DATA:
    APPLICATION NUMBER: US 08/752,182
    FILING DATE: 03-October-1996
  ATTORNEY/AGENT INFORMATION:
    NAME: Hanson, No. 6251603man D.
    REGISTRATION NUMBER: 30,946
    TELECOMMUNICATION INFORMATION:
      TELEPHONE: (212) 318-3000
      TELEFAX: (212) 752-5958
    INFORMATION FOR SEQ ID NO: 11:
      SEQUENCE CHARACTERISTICS:
        LENGTH: 18 amino acids
        TYPE: amino acid
        TOPOLOGY: linear
US-09-359-503-11

Alignment Scores:
Pred. No.:      1.21      Length:      18
Score:          18.00      Matches:      18
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match:    10.00%      Indels:      0
DB:             1          Gaps:          0

US-10-023-182-1 (1-752) x US-09-359-503-11 (1-18)

Cy      252 GCGCGGCTTCAGGCGTGAATGATGCTGCGAGATGCGGCGCCAGGGGCGCGAG 305
Db      1  GlyAlaIaSerGlyLeuValnGlyCysCysArgCysGlyAlaArgGlyProGlu 18

RESULT 5
US-09-359-503-12
Sequence 12, Application US/09359503
Patent No. 6251603
GENERAL INFORMATION:
  APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
  APPLICANT: Knuth, Alexander
  TITLE OF INVENTION: Method for Determining Status of A
  TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
  TITLE OF INVENTION: a Patient Sample
  NUMBER OF SEQUENCES: 14
  CORRESPONDENCE ADDRESS:
    ADDRESSEE: Fulbright & Jaworski, L.L.P.
    STREET: 666 Fifth Avenue
    CITY: New York City
    STATE: New York
    COUNTRY: USA
    ZIP: 10103
  COMPUTER READABLE FORM:
    MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
  COMPUTER: IBM
  OPERATING SYSTEM: PC-DOS
  SOFTWARE: WordPerfect
  CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/359,503
    FILING DATE: July 23, 1999
  CLASSIFICATION:
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 09/165,546
      FILING DATE: October 2, 1998
    PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 09/062,422
      FILING DATE: July 23, 1999
  to NY-
```


APPLICANT: Knuth, alexander
TITLE OF INVENTION: Method for Determining Status of A
TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
TITLE OF INVENTION: a Patient Sample
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6251603man D.
REGISTRATION/DOCKET NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-359-503-4

Alignment Scores:
Pred. No.: 12.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
Gaps: 0

US-10-023-182-1 (1-752) x US-09-359-503-4 (1-11)

OY 522 TCCTGTGATGATGATCAGCAGTCTTTCTG 554
|||||
Db 1 SerleuNeuMetTpIleThrGInGysPheLeu 11

RESULT 9
US-09-062-422-4
Sequence 4, Application US/09062422
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
APPLICANT: Old, Lloyd J.
TITLE OF INVENTION: ANTIBODIES WHICH BIND TO NY-ESO-1
TITLE OF INVENTION: CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
TITLE OF INVENTION: FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
TITLE OF INVENTION: THEREFROM

NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/062,422
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6252052man D.
REGISTRATION/DOCKET NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-062-422-4

Alignment Scores:
Pred. No.: 12.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
Gaps: 0

US-10-023-182-1 (1-752) x US-09-062-422-4 (1-11)

OY 522 TCCTGTGATGATGATCAGCAGTCTTTCTG 554
|||||
Db 1 SerleuNeuMetTpIleThrGInGysPheLeu 11

RESULT 10
US-08-937-263B-4
Sequence 4, Application US/08937263B
Patent No. 6274145
GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander, Knuth; Drifhout, Jan W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
TITLE OF INVENTION: ITSELF, AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM

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/
/ OPERATING SYSTEM: PC-DOS
/ SOFTWARE: WordPerfect
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/937,263B
/ FILING DATE: September 15, 1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/725,182
/ FILING DATE: October 3, 1996
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Simm, Eric, Patent Agent
/ REGISTRATION NUMBER: 40,177
/ REFERENCE/DOCKET NUMBER: LUD 5466.1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 318-3000
/ TELEFAX: (212) 752-5958
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/
US-08-937-263B-4

Alignment Scores:
Pred. No.: 12.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-08-937-263B-4 (1-11)
QY 522 TCCTGTGATGATGATCAGCAGCTTCTG 554
Db 1 SerleuMetTIpIleThrGInCysPheLeu 11

RESULT 11
US-09-166-448-79
/ Sequence 79, Application US/09166448
/ Patent No. 6291430
/ GENERAL INFORMATION:
/ APPLICANT: Chau, Pascal
/ APPLICANT: Vantomme, Valrie
/ APPLICANT: Stroobant, Vincent
/ APPLICANT: Boon-Falleur, Thierry
/ APPLICANT: van der Bruggen, Pierre
/ APPLICANT: Thielemans, Kris
/ APPLICANT: Corthals, Jurgen
/ TITLE OF INVENTION: WAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
/ FILE REFERENCE: L0461/7052
/ CURRENT APPLICATION NUMBER: US/09/166,448
/ CURRENT FILING DATE: 1998-10-05
/ NUMBER OF SEQ ID NOS: 81
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 79
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/
US-09-166-448-79

Alignment Scores:
Pred. No.: 12.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-166-448-79 (1-11)
QY 522 TCCTGTGATGATGATCAGCAGCTTCTG 554
Db 1 SerleuMetTIpIleThrGInCysPheLeu 11
```

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RESULT 12
US-09-705-160-42
/ Sequence 42, Application US/09705160
/ Patent No. 6387630
/ GENERAL INFORMATION:
/ APPLICANT: Van Baten, Nicolas
/ APPLICANT: Brasseur, Francis
/ APPLICANT: Boon-Falleur, Thierry
/ TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
/ FILE REFERENCE: LUD 5527.3-JEL/MAS
/ CURRENT APPLICATION NUMBER: US/09/705,160
/ CURRENT FILING DATE: 2001-11-02
/ PRIOR APPLICATION NUMBER: US 09/183,931
/ PRIOR FILING DATE: 1998 - 10 - 30
/ NUMBER OF SEQ ID NOS: 44
/ SEQ ID NO 42
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION:
/
US-09-705-160-42

Alignment Scores:
Pred. No.: 12.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-705-160-42 (1-11)
QY 522 TCCTGTGATGATGATCAGCAGCTTCTG 554
Db 1 SerleuMetTIpIleThrGInCysPheLeu 11

RESULT 13
US-09-440-621-1
/ Sequence 1, Application US/09440621
/ Patent No. 6417165
/ GENERAL INFORMATION:
/ APPLICANT: Valmori, Danila
/ APPLICANT: Cerottini, Jean-Charles
/ APPLICANT: Romero, Pedro
/ TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
/ FILE REFERENCE: LUD 5629
/ CURRENT APPLICATION NUMBER: US/09/440,621
/ CURRENT FILING DATE: 1999-11-15
/ EARLIER APPLICATION NUMBER: US 09/165,546
/ EARLIER FILING DATE: 1998-10-02
/ EARLIER APPLICATION NUMBER: US 09/062,422
/ EARLIER FILING DATE: 1998-04-17
/ EARLIER APPLICATION NUMBER: US 08/725,162
/ EARLIER FILING DATE: 1996-10-03
/ NUMBER OF SEQ ID NOS: 10
/ SEQ ID NO 1
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/
US-09-440-621-1

Alignment Scores:
Pred. No.: 12.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0
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US-10-023-182-1 (1-752) x US-09-440-621-1 (1-11)
QY 522 TCCTGTTGATGATGATCAGCAGTCTTCTG 554
Db 1 SerleuNeuMetriPlethInGInCySphelu 11

RESULT 14
US-09-697-884-79
Sequence 79, Application US/09697884
Patent No. 6426217
GENERAL INFORMATION:
APPLICANT: Chaux, Pascal
APPLICANT: Vantomme, Val,rie
APPLICANT: Stroppant, Vincent
APPLICANT: Boon-Pallieur, Thierry
APPLICANT: van der Bruggen, Pierre
APPLICANT: Thielemans, Kris
APPLICANT: Cortchals, Jurgen
TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
FILE REFERENCE: L0461/7052
CURRENT APPLICATION NUMBER: US/09/697,884
CURRENT FILING DATE: 2000-10-27
PRIOR APPLICATION NUMBER: 09/166,448
PRIOR FILING DATE: 1998-10-05
NUMBER OF SEQ ID NOS: 81
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 79
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-697-884-79

Alignment Scores:
Pred. No.: 12.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-697-884-79 (1-11)
QY 522 TCCTGTTGATGATGATCAGCAGTCTTCTG 554
Db 1 SerleuNeuMetriPlethInGInCySphelu 11

RESULT 15
US-09-751-798-4
Sequence 4, Application US/09751798
Patent No. 6525177
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scamhan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6525177man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-751-798-4

Alignment Scores:
Pred. No.: 12.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-751-798-4 (1-11)
QY 522 TCCTGTTGATGATGATCAGCAGTCTTCTG 554
Db 1 SerleuNeuMetriPlethInGInCySphelu 11

RESULT 16
US-09-344-040C-130
Sequence 130, Application US/09344040C
Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfrendeschuh, Michael
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/09/344,040C
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 130
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-344-040C-130

Alignment Scores:
Pred. No.: 12.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-130 (1-11)
QY 522 TCCTGTTGATGATGATCAGCAGTCTTCTG 554

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Db      1 SerLeuMetTrrPleThrGlnCysPheLeu 11
|||||
RESULT 17
US-09-574-749B-33
; Sequence 33, Application US/09574749B
; Patent No. 6548299
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADDEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/09/574,749B
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-09-574-749B-33

Alignment Scores:
Pred. No.:      12.1      Length:      11
Score:          11.00     Matches:      11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    6.11%     Indels:      0
DB:             1         Gaps:          0

US-10-023-182-1 (1-752) x US-09-574-749B-33 (1-11)
QY      522 TCCTGTGATGATGATCAGCAGTCTTCTG 554
Db      1 SerLeuMetTrrPleThrGlnCysPheLeu 11
|||||
RESULT 18
US-09-676-005B-1
; Sequence 1, Application US/09676005B
; Patent No. 6605711
; GENERAL INFORMATION:
; APPLICANT: Valmorri, Daniela
; APPLICANT: Cerrotini, Jean, Charels
; APPLICANT: Romero, Pedro
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629.2
; CURRENT APPLICATION NUMBER: US/09/676,005B
; CURRENT FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US09/514,036
; PRIOR FILING DATE: 2000-02-05
; PRIOR APPLICATION NUMBER: US09/440,621
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 09/165,546
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: US 09/062,422
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 08/725,162
; PRIOR FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 1
; LENGTH: 11
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; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-676-005B-1

Alignment Scores:
Pred. No.:      12.1      Length:      11
Score:          11.00     Matches:      11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    6.11%     Indels:      0
DB:             1         Gaps:          0

US-10-023-182-1 (1-752) x US-09-676-005B-1 (1-11)
QY      522 TCCTGTGATGATGATCAGCAGTCTTCTG 554
Db      1 SerLeuMetTrrPleThrGlnCysPheLeu 11
|||||
RESULT 19
US-09-833-039A-130
; Sequence 130, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfeundschnuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 130
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-130

Alignment Scores:
Pred. No.:      12.1      Length:      11
Score:          11.00     Matches:      11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    6.11%     Indels:      0
DB:             1         Gaps:          0

US-10-023-182-1 (1-752) x US-09-833-039A-130 (1-11)
QY      522 TCCTGTGATGATGATCAGCAGTCTTCTG 554
Db      1 SerLeuMetTrrPleThrGlnCysPheLeu 11
|||||
RESULT 20
US-09-359-503-7
; Sequence 7, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, Alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
```


CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/359,503
FILING DATE: July 23, 1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/165,546
FILING DATE: October 2, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE: April 17, 1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/937,263
FILING DATE: September 15, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/752,182
FILING DATE: 03-October-1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. 6251603man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-359-503-7

Alignment Scores:
Pred. No.: 16.9 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-359-503-7 (1-10)

QY 525 CTGTTGATGTGATCAGCGAGTCTTCTG 554
Db 1 LeuLeuMettrIlethnGlnCyRheLeu 10

RESULT 21
US-09-344-040C-126
Sequence 126, Application US/09344040C
Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
APPLICANT: Ramenese, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05

NUMBER OF SEQ ID NOS: 132
SEQ ID NO 126
LENGTH: 10
TYPE: PR
ORGANISM: Homo sapiens
US-09-344-040C-126

Alignment Scores:
Pred. No.: 16.9 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-126 (1-10)

QY 168 GCCACGGCGCGGAGGTCCCGGCGCGCA 197
Db 1 AlaThrGlyGlyArgGlyProArgGlyAla 10

RESULT 22
US-09-344-040C-127
Sequence 127, Application US/09344040C
Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
APPLICANT: Ramenese, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 127
LENGTH: 10
TYPE: PR
ORGANISM: Homo sapiens
US-09-344-040C-127

Alignment Scores:
Pred. No.: 16.9 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-127 (1-10)

QY 228 GCGCGCCCGCGGCGTCCGATGCGGCGCG 257
Db 1 GlyAlaProArgGlyProHISGlyGlyAla 10

RESULT 23
US-09-344-040C-128
Sequence 128, Application US/09344040C
Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
APPLICANT: Ramenese, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini

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; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 128
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-128

Alignment Scores:
Pred. No.: 16.9 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-128 (1-10)
QY 363 CTGCCCGAGAGCTGCGCCGAGATGCC 392
DB 1 LeuAlaArgArgSerLeuAlaGlnAspAla 10

RESULT 24
US-09-344-040C-129
; Sequence 129, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 129
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-129

Alignment Scores:
Pred. No.: 16.9 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-129 (1-10)
QY 537 ATCAGCAGTGTCTTCTGCGCGTGTG 566
DB 1 IleThrGlnCysPheLeuProValPheLeu 10

RESULT 25
US-09-676-005B-11
```

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; Sequence 11, Application US/09676005B
; Patent No. 6605711
; GENERAL INFORMATION:
; APPLICANT: Valmori, Danila
; APPLICANT: Cerrito, Jean, Charels
; APPLICANT: Romero, Pedro
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629.2
; CURRENT APPLICATION NUMBER: US/09/676,005B
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: US09/514,036
; PRIOR FILING DATE: 2000-02-05
; PRIOR APPLICATION NUMBER: US09/440,621
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 09/165,546
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: US 09/062,422
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 08/725,162
; PRIOR FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 11
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-676-005B-11

Alignment Scores:
Pred. No.: 16.9 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-676-005B-11 (1-10)
QY 522 TCCTGTGATGTGATCATCGCAGTGT 551
DB 1 SerLeuMetTrpIleThrGlnCysPhe 10

RESULT 26
US-09-833-039A-126
; Sequence 126, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 126
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-126

Alignment Scores:
Pred. No.: 16.9 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
```

Query Match:	5.56%	Indels:	0
DB:	1	Gaps:	0
US-10-023-182-1 (1-752) x US-09-833-039A-126 (1-10)			
Qy	168	GCACGCGCGGAGAGTCCCGGCGCGCA	197
Db	1	AlaThrGlyArgGlyProArgGlyAla	10
RESULT 27			
US-09-833-039A-127			
Sequence 127, Application US/09833039A			
Patent No. 6673350			
GENERAL INFORMATION:			
APPLICANT: Tuireci, Ozlem			
APPLICANT: Sahin, Ugur			
APPLICANT: Pfeundschn, Michael			
TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof			
FILE REFERENCE: LUD 5622.1			
CURRENT APPLICATION NUMBER: US/09/833,039A			
CURRENT FILING DATE: 2001-04-12			
PRIOR APPLICATION NUMBER: US 09/409,455			
PRIOR FILING DATE: 1999-06-25			
PRIOR APPLICATION NUMBER: US 09/344,040			
PRIOR FILING DATE: 1999-06-26			
PRIOR APPLICATION NUMBER: US 09/105,839			
PRIOR FILING DATE: 1998-06-26			
NUMBER OF SEQ ID NOS: 131			
SOFTWARE: PatentIn version 3.2			
SEQ ID NO 128			
LENGTH: 10			
TYPE: PRT			
ORGANISM: Homo sapiens			
US-09-833-039A-127			
Alignment Scores:			
Pred. No.:	16.9	Length:	10
Score:	100.00	Matches:	10
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	5.56%	Indels:	0
DB:	1	Gaps:	0
US-10-023-182-1 (1-752) x US-09-833-039A-127 (1-10)			
Qy	228	GGCGCCCGCGGGTCCGCATGGCGGCGCG	257
Db	1	GlyAlaProArgGlyProHisGlyAla	10
RESULT 28			
US-09-833-039A-128			
Sequence 128, Application US/09833039A			
Patent No. 6673350			
GENERAL INFORMATION:			
APPLICANT: Tuireci, Ozlem			
APPLICANT: Sahin, Ugur			
APPLICANT: Pfeundschn, Michael			
TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof			
FILE REFERENCE: LUD 5622.1			
CURRENT APPLICATION NUMBER: US/09/833,039A			
CURRENT FILING DATE: 2001-04-12			
PRIOR APPLICATION NUMBER: US 09/409,455			
PRIOR FILING DATE: 1999-06-25			
PRIOR APPLICATION NUMBER: US 09/344,040			
PRIOR FILING DATE: 1999-06-26			
PRIOR APPLICATION NUMBER: US 09/105,839			
PRIOR FILING DATE: 1998-06-26			
NUMBER OF SEQ ID NOS: 131			
SOFTWARE: PatentIn version 3.2			
SEQ ID NO 128			
LENGTH: 10			
TYPE: PRT			
ORGANISM: Homo sapiens			

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US-09-833-039A-128
Alignment Scores:
Pred. NO.: 16.9 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039A-128 (1-10)
OY 363 CTGCGCCGAGAGAGCTTGGCCGAGATGCC 392
Db 1 LeuAlaIrgArGserLeuAlaGlnAspAla 10

RESULT 29
US-09-833-039A-129
Sequence 129, Application US/09833039A
Patent No. 6673350
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfrendeschuh, Michael
TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
FILE REFERENCE: LUD 5622.1
CURRENT APPLICATION NUMBER: US/09/833,039A
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 09/409,455
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/344,040
PRIOR FILING DATE: 1999-06-26
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
NUMBER OF SEQ ID NOS: 131
SOFTWARE: PatentIn version 3.2
SEQ ID NO 129
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-039A-129

Alignment Scores:
Pred. No.: 16.9 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039A-129 (1-10)
OY 537 ATCAGCAGAGCTTTCGCGCGCTTTTG 566
Db 1 IleThrGlnCysPheLeuProValPheLeu 10

RESULT 30
US-09-183-931-43
Sequence 43, Application US/09183931C
Patent No. 6210886
GENERAL INFORMATION:
APPLICANT: Van Baren, Nicolas
APPLICANT: Brasseur, Francis
APPLICANT: Boon-Falloux, Thierry
TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
FILE REFERENCE: LUD 5527.1-JEL/ES
CURRENT APPLICATION NUMBER: US/09/183,931C
CURRENT FILING DATE: 2000-02-28
EARLIER APPLICATION NUMBER: US 09/018,422
EARLIER FILING DATE: 1998 - 02 - 04
NUMBER OF SEQ ID NOS: 44
SEQ ID NO 43

```

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/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION:
US-09-183-931-43

Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%    Conservative: 9
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 5.00%              Indels: 0
DB: 1                       Gaps: 0

US-10-023-182-1 (1-752) x US-09-183-931-44 (1-9)

QY 522 TCCTGTGATGTGATCAGCAGTGC 548
    |||||||
Db 1 SerleuSemettriplethrInGncys 9

RESULT 31
US-09-183-931-44
; Sequence 44, Application US/09183931C
; Patent No. 6210886
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
; FILE REFERENCE: LOD 5527.1-UEL/ES
; CURRENT APPLICATION NUMBER: US/09/183,931C
; EARLIER FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: US 09/018,422
; EARLIER FILING DATE: 1998 - 02 - 04
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-183-931-44

Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%    Conservative: 9
Best Local Similarity: 100.00%    Mismatches: 0
Query Match: 5.00%              Indels: 0
DB: 1                       Gaps: 0

US-10-023-182-1 (1-752) x US-09-183-931-44 (1-9)

QY 516 CAGCTTCCCTGTGATGTGATCAGC 542
    |||||||
Db 1 GinleuSerleuSemettriplethr 9

RESULT 32
US-09-359-503-5
; Sequence 5, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
; APPLICANT: Knuth, Alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Antibodies
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESS: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue

```

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1 CITY: New York City
2 STATE: New York
3 COUNTRY: USA
4 ZIP: 10103
5
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
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```


NAME: Hanson, No. 6252052man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-062-422-6

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-062-422-6 (1-9)

QY 516 CAGCTTCCCTGTGATGCAGCAG 542
Db 1 GinLeuSerLeuMetTrieThr 9

RESULT 36
US-08-937-263B-5
Sequence 5, Application US/08937263B
Patent No. 6274145

GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander, Knuth; Drifflout, Jan W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
FILING DATE: September 15, 1997
APPLICATION NUMBER: US/08/937,263B
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Simm, Eric, Patent Agent
REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-937-263B-5

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-08-937-263B-6 (1-9)

QY 516 CAGCTTCCCTGTGATGCAGCAG 542
Db 1 GinLeuSerLeuMetTrieThr 9

RESULT 37
US-08-937-263B-6
Sequence 6, Application US/08937263B
Patent No. 6274145

GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander, Knuth; Drifflout, Jan W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
FILING DATE: September 15, 1997
APPLICATION NUMBER: US/08/937,263B
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Simm, Eric, Patent Agent
REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-937-263B-6

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-08-937-263B-5 (1-9)

QY 522 TCCTGTGATGCAGCAGTGC 548
Db 1 SerLeuMetTrieThrGlnCys 9

RESULT 38
US-08-166-448-80
Sequence 80, Application US/09166448

Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-08-937-263B-5 (1-9)

QY 522 TCCTGTGATGCAGCAGTGC 548
Db 1 SerLeuMetTrieThrGlnCys 9

RESULT 37
US-08-937-263B-6
Sequence 6, Application US/08937263B
Patent No. 6274145

GENERAL INFORMATION:
APPLICANT: Chen, Yao-Tseng; Scanlan, Matthew;
APPLICANT: Gure, Ali; Old, Lloyd J.; Jager, Elke;
APPLICANT: Alexander, Knuth; Drifflout, Jan W.
TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE
TITLE OF INVENTION: ENCODING CANCER ASSOCIATED ANTIGEN, THE ANTIGEN
NUMBER OF SEQUENCES: 8
CURRENT APPLICATION DATA:
FILING DATE: September 15, 1997
APPLICATION NUMBER: US/08/937,263B
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Simm, Eric, Patent Agent
REGISTRATION NUMBER: 40,177
REFERENCE/DOCKET NUMBER: LUD 5466.1
TELEPHONE: (212) 318-3000
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-937-263B-6

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-08-937-263B-6 (1-9)

QY 516 CAGCTTCCCTGTGATGCAGCAG 542
Db 1 GinLeuSerLeuMetTrieThr 9

RESULT 38
US-08-166-448-80
Sequence 80, Application US/09166448

Patent No. 6291430
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/166,448
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-448-80

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-166-448-80 (1-9)

OY 522 TCCTGTGATGTGATCAGCAGTCG 548

Db 1 SerleuSeuMetTIpIeThrGInCyS 9

RESULT 39
US-09-166-448-81
; Sequence 81, Application US/09166448
; Patent No. 6291430
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vantomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Corthals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/166,448
; CURRENT FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 81
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-166-448-81

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-166-448-81 (1-9)

OY 516 CAGCTTCCCTGTGATGTGATCAGC 542

Db 1 GinleuSeuMetTIpIeThr 9

RESULT 40
US-09-705-160-43
; Sequence 43, Application US/09705160
; Patent No. 6387630
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; FILE REFERENCE: LUD 5527.3-JEL/MAS
; CURRENT APPLICATION NUMBER: US/09/705,160
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 09/183,931
; PRIOR FILING DATE: 1998 - 10 - 30
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO: 43
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-705-160-43

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-705-160-43 (1-9)

OY 522 TCCTGTGATGTGATCAGCAGTCG 548

Db 1 SerleuSeuMetTIpIeThrGInCyS 9

RESULT 41
US-09-705-160-44
; Sequence 44, Application US/09705160
; Patent No. 6387630
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; FILE REFERENCE: LUD 5527.3-JEL/MAS
; CURRENT APPLICATION NUMBER: US/09/705,160
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: US 09/183,931
; PRIOR FILING DATE: 1998 - 10 - 30
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO: 44
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION:
US-09-705-160-44

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-705-160-44 (1-9)

OY 516 CAGCTTCCCTGTGATGTGATCAGC 542

Db 1 GlnLeuSerLeuMetTrpIleThr 9
|||||
RESULT 42
US-09-440-621-2
; Sequence 2, Application US/09440621
; Patent No. 6417165
; GENERAL INFORMATION:
; APPLICANT: Valmori, Danila
; APPLICANT: Cerottini, Jean-Charles
; APPLICANT: Romero, Pedro
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629
; CURRENT APPLICATION NUMBER: US/09/440,621
; EARLIER FILING DATE: 1999-11-15
; EARLIER APPLICATION NUMBER: US 09/165,546
; EARLIER FILING DATE: 1998-10-02
; EARLIER APPLICATION NUMBER: US 09/062,422
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: US 08/725,162
; EARLIER FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-440-621-2
Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-09-440-621-2 (1-9)
QY 522 TCCTGTGATGTGATGATCAGCAGTGC 548
|||||
Db 1 SerLeuMetTrpIleThrGlnCys 9
|||||
RESULT 43
US-09-440-621-3
; Sequence 3, Application US/09440621
; Patent No. 6417165
; GENERAL INFORMATION:
; APPLICANT: Valmori, Danila
; APPLICANT: Cerottini, Jean-Charles
; APPLICANT: Romero, Pedro
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629
; CURRENT APPLICATION NUMBER: US/09/440,621
; EARLIER FILING DATE: 1999-11-15
; EARLIER APPLICATION NUMBER: US 09/165,546
; EARLIER FILING DATE: 1998-10-02
; EARLIER APPLICATION NUMBER: US 09/062,422
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: US 08/725,162
; EARLIER FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-440-621-3
Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-09-440-621-3 (1-9)
QY 516 CAGCTTCCCTGTGATGTGATCAGC 542
|||||
Db 1 GlnLeuSerLeuMetTrpIleThr 9
|||||
RESULT 44
US-09-697-884-80
; Sequence 80, Application US/09697884
; Patent No. 6426217
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vantombe, Val,rie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/697,884
; EARLIER FILING DATE: 2000-10-27
; EARLIER APPLICATION NUMBER: 09/166,448
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-697-884-80
Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-09-697-884-80 (1-9)
QY 522 TCCTGTGATGTGATGATCAGCAGTGC 548
|||||
Db 1 SerLeuMetTrpIleThrGlnCys 9
|||||
RESULT 45
US-09-697-884-81
; Sequence 81, Application US/09697884
; Patent No. 6426217
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vantombe, Val,rie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/09/697,884
; EARLIER FILING DATE: 2000-10-27
; EARLIER APPLICATION NUMBER: 09/166,448
; EARLIER FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 9
; TYPE: PRT


```
; ORGANISM: Homo sapiens
US-09-697-884-81

Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-09-697-884-81 (1-9)

QY      516 CAGCTTCCCTGTGATGTGATGCACG 542
Db      1 GlnleuSerleuMettrpIleThr 9

RESULT 46
US-09-670-456A-1
; Sequence 1, Application US/09670456A
; Patent No. 6506875
; GENERAL INFORMATION:
; LUD-5668-PCT
; APPLICANT: Gnjatic, Sacha
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA-C MOLECULES AND USES
; FILE REFERENCE: LUD 5668
; CURRENT APPLICATION NUMBER: US/09/670,456A
; CURRENT FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-670-456A-1

Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-09-670-456A-1 (1-9)

QY      522 TCCCTGTGATGTGATGCACGAGTGC 548
Db      1 SerleuMettrpIleThrGlnGly 9

RESULT 47
US-09-670-456A-2
; Sequence 2, Application US/09670456A
; Patent No. 6506875
; GENERAL INFORMATION:
; LUD-5668-PCT
; APPLICANT: Gnjatic, Sacha
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA-C MOLECULES AND USES
; FILE REFERENCE: LUD 5668
; CURRENT APPLICATION NUMBER: US/09/670,456A
; CURRENT FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-670-456A-2

Alignment Scores:
Pred. No.: 78          Length: 9
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```
Score: 9.00           Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-09-670-456A-2 (1-9)

QY      327 CTGGCGATGCTTTCGGACACCCATG 353
Db      1 LeuAlaMetProPheAlaIrnProMet 9

RESULT 48
US-09-670-456A-3
; Sequence 3, Application US/09670456A
; Patent No. 6506875
; GENERAL INFORMATION:
; LUD-5668-PCT
; APPLICANT: Gnjatic, Sacha
; APPLICANT: Old, Lloyd J.
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA-C MOLECULES AND USES
; FILE REFERENCE: LUD 5668
; CURRENT APPLICATION NUMBER: US/09/670,456A
; CURRENT FILING DATE: 2001-09-26
; NUMBER OF SEQ ID NOS: 5
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-670-456A-3

Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-09-670-456A-3 (1-9)

QY      291 GCCAGGGCGCCGAGAGCCGCTGCTT 317
Db      1 AlaArgGlyProGlnSerAlaGlyLeu 9

RESULT 49
US-09-751-798-5
; Sequence 5, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
```

```

; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6525177man D.
; REGISTRATION NUMBER: 30,946
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-5

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-751-798-5 (1-9)
QY 522 TCCTGTGATGTGATGCAGCAGTGC 548
DB 1 SerLeuMetTrpIleThrGlnCys 9

RESULT 50
US-09-751-798-6
; Sequence 6, Application US/09751798
; Patent No. 6525177
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
; APPLICANT: Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; TITLE OF INVENTION: Associated Proteins, Uses Thereof,
; TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
; TITLE OF INVENTION: Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/751,798
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 6525177man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3

```

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; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-6

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-751-798-6 (1-9)
QY 516 CAGCTTCCTGTGATGTGATCAGC 542
DB 1 GlnLeuSerLeuMetTrpIleThr 9

RESULT 51
US-09-344-040C-19
; Sequence 19, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determini
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene at
; FILE REFERENCE: LUD 5556.1
; CURRENT FILING DATE: 1999-06-25
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-19

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-19 (1-9)
QY 309 CGCCTGCTTGATGTCTACCTGCATG 335
DB 1 ArgLeuGlnIlePheTyrLeuAlaMet 9

RESULT 52
US-09-344-040C-20
; Sequence 20, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael

```

```

; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344, 040C
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105, 839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-20

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-20 (1-9)

OY 375 AGCTGCGCCAGATGCCACCGCTT 401
Db 1 SerleuaIaGlnAaPAlaProPleu 9

RESULT 53
US-09-344-040C-115
; Sequence 115, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendeschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344, 040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 09/105, 839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 115
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-115

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-115 (1-9)

OY 495 TCATCAGCTCTCTGTCTCCAGACGCTT 521
Db 1 SerleSerSerCylleuGlnGlnleu 9
```

```

US-09-344-040C-116
; Sequence 116, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendeschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344, 040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 09/105, 839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-116

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-116 (1-9)

OY 72 GGCACAGGGGTTGACGGCGATGCT 98
Db 1 GLythrgIyglSerThrngIyAspAla 9

RESULT 55
US-09-344-040C-117
; Sequence 117, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendeschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344, 040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 09/105, 839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 117
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-117

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
```

```
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-09-344-040C-117 (1-9)

QY 207 AGGCGCTCGGGCCGAGAGAGCGCC 233
DB 1 ArgAlaSerGlyProGlyGlyAla 9

RESULT 56
US-09-344-040C-118
; Sequence 118, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendeschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 118
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-118

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-09-344-040C-118 (1-9)

QY 288 GGGCGCAGGGGCGGAGAGCGCGCTG 314
DB 1 GlyAlaArgGlyProGlySerArgLeu 9

RESULT 57
US-09-344-040C-119
; Sequence 119, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendeschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 119
```

```
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-119

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-09-344-040C-119 (1-9)

QY 342 GCGACACCCATGACAGAGAGCTGACC 368
DB 1 AlaThrProMetGluAlaGluLeuAla 9

RESULT 58
US-09-344-040C-120
; Sequence 120, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendeschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determini
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 120
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-344-040C-120

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-09-344-040C-120 (1-9)

QY 429 TTCACGTGTCCGCAACATGACTGACT 455
DB 1 PheThrValSerGlyAsnIleLeuThr 9

RESULT 59
US-09-344-040C-121
; Sequence 121, Application US/09344040C
; Patent No. 6548064
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendeschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determini
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/09/344,040C
; CURRENT FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 121
```

```
FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 121
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-344-040C-121

Alignment Scores:
Pred. No.: 78
Score: 9.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.00%
DB: 1
Length: 9
Matches: 9
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-121 (1-9)

QY 462 CTGACTGCTGCAGACCGCCACTG 488
DB 1 LeuThrAlaAlaAspHisArgGlnLeu 9

RESULT 60
US-09-344-040C-122
Sequence 122, Application US/09344040C
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 122
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-344-040C-122

Alignment Scores:
Pred. No.: 78
Score: 9.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.00%
DB: 1
Length: 9
Matches: 9
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-122 (1-9)

QY 516 CAGCTTCCTGTTGATGTGATCAGC 542
DB 1 GlnLeuSerLeuLeuMetTrpIleThr 9

RESULT 61
US-09-344-040C-123
Sequence 123, Application US/09344040C
Patent No. 6548064
```

```
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 123
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-344-040C-123

Alignment Scores:
Pred. No.: 78
Score: 9.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.00%
DB: 1
Length: 9
Matches: 9
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-123 (1-9)

QY 528 TTGATGTGATCAGCAGTGTCTTG 554
DB 1 LeuMetTrpIleThrGlnCysPheLeu 9

RESULT 62
US-09-344-040C-124
Sequence 124, Application US/09344040C
Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 124
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-344-040C-124

Alignment Scores:
Pred. No.: 78
Score: 9.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.00%
DB: 1
Length: 9
Matches: 9
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-124 (1-9)
```

QY 339 TTCGCACACCCATGAGCAGCCTG 365
DB 1 PhealatrPrmetGluablaetlueu 9

RESULT 63
US-09-344-040C-125
Sequence 125, Application US/09344040C
Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfeundschnuh, Michael
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determining Presence of an SSX Gene, Peptides Derived From Said SSX Gene
TITLE OF INVENTION: Gene, and Uses Thereof
FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 125
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-344-040C-125

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-125 (1-9)

QY 432 ACTGTGTCGGCAGACACTGACTATC 458
DB 1 ThrValSerGlyAsnIleuThrIle 9

RESULT 64
US-09-344-040C-131
Sequence 131, Application US/09344040C
Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfeundschnuh, Michael
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determining Presence of an SSX Gene, Peptides Derived From Said SSX Gene
TITLE OF INVENTION: Gene, and Uses Thereof
FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 131
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-344-040C-131

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-131 (1-9)

QY 522 TCCTGTTGATGTGATCAGCAGTGC 548
DB 1 SerIleuMetTrpIleuMetTrpIleuGlnCys 9

RESULT 65
US-09-344-040C-132
Sequence 132, Application US/09344040C
Patent No. 6548064
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfeundschnuh, Michael
APPLICANT: Ramensee, Hans Georg
APPLICANT: Stevanovic, Stefan
TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determining Presence of an SSX Gene, Peptides Derived From Said SSX Gene
TITLE OF INVENTION: Gene, and Uses Thereof
FILE REFERENCE: LUD 5556.1
CURRENT APPLICATION NUMBER: US/09/344,040C
CURRENT FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 132
SEQ ID NO 132
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-344-040C-132

Alignment Scores:
Pred. No.: 78 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-344-040C-132 (1-9)

QY 516 CAGCTTCCCTGTGATGATGATCAGC 542
DB 1 GlnIleuSerIleuLeuMetTrpIleuThr 9

RESULT 66
US-09-574-749B-34
Sequence 34, Application US/09574749B
Patent No. 6548299
GENERAL INFORMATION:
APPLICANT: ROSENZWEIG, Michael
APPLICANT: PYKETT, Mark J.
APPLICANT: SCADDEN, David T.
APPLICANT: POZNANSKY, Mark C.
TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
FILE REFERENCE: C1005/7012/KA/ERG
CURRENT APPLICATION NUMBER: US/09/574,749B
CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US 60/107,972
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: PCT/US99/26795

```

; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-09-574-749B-34

Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%     Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-09-574-749B-34 (1-9)

QY 522 TCCTGTGATGTGATCGACGAGTGC 548
DB 1 SerleuMettripleThrcInCys 9

RESULT 67
US-09-574-749B-35
; Sequence 35, Application US/09574749B
; Patent No. 6548299
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; TITLE OF INVENTION: DEVICES
; FILE REFERENCE: C1005/7012/Ka/ERG
; CURRENT APPLICATION NUMBER: US/09/574,749B
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-09-574-749B-35

Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%     Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-09-574-749B-35 (1-9)

QY 516 CAGCTTTCCTGTGATGTGATCGACG 542
DB 1 GinleuSerleuMettripleThrcInCys 9

RESULT 68
```

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US-09-676-005B-2
; Sequence 2, Application US/09676005B
; Patent No. 6605711
; GENERAL INFORMATION:
; APPLICANT: Valmori, Danila
; APPLICANT: Cerrocin, Jean, Charels
; APPLICANT: Romero, Pedro
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629.2
; CURRENT APPLICATION NUMBER: US/09/676,005B
; CURRENT FILING DATE: 2000-09-29
; PRIOR FILING DATE: 2000-02-05
; PRIOR APPLICATION NUMBER: US09/440,621
; PRIOR FILING DATE: 2000-02-05
; PRIOR APPLICATION NUMBER: US 09/165,546
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: US 09/062,422
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 08/725,162
; PRIOR FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-676-005B-2

Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%     Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-09-676-005B-2 (1-9)

QY 522 TCCTGTGATGTGATCGACGAGTGC 548
DB 1 SerleuMettripleThrcInCys 9

RESULT 69
US-09-676-005B-3
; Sequence 3, Application US/09676005B
; Patent No. 6605711
; GENERAL INFORMATION:
; APPLICANT: Valmori, Danila
; APPLICANT: Cerrocin, Jean, Charels
; APPLICANT: Romero, Pedro
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629.2
; CURRENT APPLICATION NUMBER: US/09/676,005B
; CURRENT FILING DATE: 2000-09-29
; PRIOR FILING DATE: 2000-02-05
; PRIOR APPLICATION NUMBER: US09/514,036
; PRIOR FILING DATE: 2000-02-05
; PRIOR APPLICATION NUMBER: US09/440,621
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 09/165,546
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: US 09/062,422
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 08/725,162
; PRIOR FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 27
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
US-09-676-005B-3
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Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%          Indels: 0
DB: 1                  Gaps: 0
US-10-023-182-1 (1-752) x US-09-676-005B-3 (1-9)

Qy      516 CAGCTTCCTGTTGATGATGATGATCAGC 542
Db      1 GlnLeuSerLeuMetIrrPilethr 9

RESULT 70
US-09-833-039A-19
; Sequence 19, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfeundschnh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-19

Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%          Indels: 0
DB: 1                  Gaps: 0
US-10-023-182-1 (1-752) x US-09-833-039A-19 (1-9)

Qy      309 GCCTGCTTGAGTTCTACTCGCCATG 335
Db      1 ArgLeuLeuGluPheTyrLeuAlaMet 9

RESULT 71
US-09-833-039A-20
; Sequence 20, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfeundschnh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
```

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-20

Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%          Indels: 0
DB: 1                  Gaps: 0
US-10-023-182-1 (1-752) x US-09-833-039A-20 (1-9)

Qy      375 AGCTGGCCGAGATGCCCGCCGCTT 401
Db      1 SerLeuAlaGlnAspAlaProIleu 9

RESULT 72
US-09-833-039A-115
; Sequence 115, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfeundschnh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 115
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-115

Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%          Indels: 0
DB: 1                  Gaps: 0
US-10-023-182-1 (1-752) x US-09-833-039A-115 (1-9)

Qy      495 TCATCAGCTCCTGATCCAGCAGCTT 521
Db      1 SerLeuSerCysLeuGlnGlnLeu 9

RESULT 73
US-09-833-039A-116
; Sequence 116, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfeundschnh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; PRIOR FILING DATE: 2001-04-12
```



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; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-116

Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00% Conservative: 9
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%     Indels: 0
DB: 1                 Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039A-116 (1-9)

OY 72 GGCACAGGGGCTTCGACGGCGATGCT 98
Db 1 G|YThrg|Yg|Yse|ThnG|YAsp|Ala 9

RESULT 74
US-09-833-039A-117
; Sequence 117, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 117
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-117

Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00% Conservative: 9
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%     Indels: 0
DB: 1                 Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039A-117 (1-9)

OY 207 AGGGCTTCGGGGCCGGGAGGAGCGGCC 233
Db 1 ArglaserGlyProGlyGlyGlyAla 9

RESULT 75
US-09-833-039A-118
; Sequence 118, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
```

```
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 118
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-118

Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00% Conservative: 9
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%     Indels: 0
DB: 1                 Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039A-118 (1-9)

OY 288 GGGGCGAGGGGCGCGAGAGCGGCTG 314
Db 1 G|YAla|Arg|G|YProG|Ins|Arg|Leu 9

RESULT 76
US-09-833-039A-119
; Sequence 119, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 119
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-119

Alignment Scores:
Pred. No.: 78          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00% Conservative: 9
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%     Indels: 0
DB: 1                 Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039A-119 (1-9)

OY 342 GGCACACCATGGAAGCAGAGCTGGCC 368
Db 1 G|YAla|Arg|G|YProG|Ins|Arg|Leu 9
```

```
Db          1 AlathrPrometGluAlaGluLeuAla 9

RESULT 77
US-09-833-039A-120
; Sequence 120, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfeundschnuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 120
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-120

Alignment Scores:
Pred. No.:          78          Length:          9
Score:              9.00        Matches:          9
Percent Similarity: 100.00%     Conservative:    0
Best Local Similarity: 100.00%  Mismatches:       0
Query Match:        5.00%       Indels:           0
DB:                  1          Gaps:              0

US-10-023-182-1 (1-752) x US-09-833-039A-120 (1-9)

Qy          429 TTCACGTGTCCGCAACATCTGACT 455
Db          1 PhetrhValSerGlyAsnIleLeuThr 9

RESULT 78
US-09-833-039A-122
; Sequence 122, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfeundschnuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 122
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-122

Alignment Scores:
Pred. No.:          78          Length:          9
Score:              9.00        Matches:          9
Percent Similarity: 100.00%     Conservative:    0
Best Local Similarity: 100.00%  Mismatches:       0
Query Match:        5.00%       Indels:           0
DB:                  1          Gaps:              0

US-10-023-182-1 (1-752) x US-09-833-039A-120 (1-9)
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```
Query Match:          5.00%      Indels:          0
DB:                    1          Gaps:              0

US-10-023-182-1 (1-752) x US-09-833-039A-122 (1-9)

Qy          516 CAGCTTCCCTGTTGATGTGATCAGC 542
Db          1 GlnLeuSerIleLeuMetTrpIleThr 9

RESULT 79
US-09-833-039A-123
; Sequence 123, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfeundschnuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-123

Alignment Scores:
Pred. No.:          78          Length:          9
Score:              9.00        Matches:          9
Percent Similarity: 100.00%     Conservative:    0
Best Local Similarity: 100.00%  Mismatches:       0
Query Match:        5.00%       Indels:           0
DB:                  1          Gaps:              0

US-10-023-182-1 (1-752) x US-09-833-039A-123 (1-9)

Qy          528 TTGATGTGATCAGCAGTGTCTTG 554
Db          1 LeuMetTrpIleThrGlnCysPheLeu 9

RESULT 80
US-09-833-039A-124
; Sequence 124, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfeundschnuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 124
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-124
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Query Match: 5.00%
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Length: 9
Matches: 9
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

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QY 339 TTCGACACCCATGAGACAGCTG 365
DB 1 PhealathrproMetGluAlaGluLeu 9

RESULT 81
US-09-833-039A-125
; Sequence 125, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 125
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-125

Alignment Scores:
Pred. No.: 78
Score: 9.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.00%
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Length: 9
Matches: 9
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RESULT 82
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; Sequence 131, Application US/09833039A
; Patent No. 6673350
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039A
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-26
; PRIOR APPLICATION NUMBER: US 09/105,839
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; PRIOR FILING DATE: 1998-06-26
; NUMBER OF SEQ ID NOS: 131
; SOFTWARE: PatentIn version 3.2
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; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039A-131

Alignment Scores:
Pred. No.: 78
Score: 9.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.00%
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Length: 9
Matches: 9
Conservative: 0
Mismatch: 0
Indels: 0
Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039A-131 (1-9)
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Job time : 1 secs
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Run on: July 21, 2004, 11:05:41 ; Search time 0.5 Seconds
(without alignments)
4.378 Million cell updates/sec

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Fgapop 6.0 , Fgapext 7.0
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Searched: 168 segs, 2027 residues

Total number of hits satisfying chosen parameters: 336

Minimum DB seq length: 5
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 178 summaries

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and is derived by analysis of the total score distribution.

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ALIGNMENTS

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; Sequence 1400, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296, 734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1400
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 2
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Score: 30.00 Matches: 30
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
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; Sequence 1402, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296, 734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1402

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; LENGTH: 30
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; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOla segment 3
US-10-296-734-1402

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Best Local Similarity: 100.00% Mismatches: 0
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; Sequence 1404, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1404
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
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US-10-296-734-1404

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; Sequence 1406, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
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; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1406
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
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US-10-296-734-1406

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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    16.67%   Indels:      0
DB:             1       Gaps:        0

US-10-023-182-1 (1-752) x US-10-296-734-1406 (1-30)

QY      228 GCGCGCCCGCGGCTCCGATGCGGCGCGCTTCAGTGAATGATGCTGAGATGC 287
      |||
Db       1 GlyAlaProArgGlyProHisGlyGlyAlaAlaSerGlyLeuHisGlyCysArgCys 20
      |||
QY      288 GCGGCACAGGCGCGCGAGAGCGGCTGCTT 317
      |||
Db       21 GlyAlaArgGlyProGlySerArgLeuLeu 30
      |||

RESULT 5
US-10-296-734-1408
; Sequence 1408, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1408
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOla segment 6
US-10-296-734-1408

Alignment Scores:
Pred. No.:      3.61      Length:      30
Score:          30.00     Matches:      30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    16.67%   Indels:      0
DB:             1       Gaps:        0

US-10-023-182-1 (1-752) x US-10-296-734-1408 (1-30)

QY      273 GGATGCTGCAGATGCGGCGCGACAGGCGCGGCTTCGTTGAGTTCTACTGCGC 332
      |||
Db       1 GlyCysCysArgCysGlyAlaAlaArgGlyProGlySerArgLeuGluPheTyrLeuAla 20
      |||
QY      333 ATGCTTCGCGCACCCATGAGAGAGAG 362
      |||
```

Db 21 NetPropeAlaThrProMetGluAlaGlu 30

RESULT 6
US-10-296-734-1410
; Sequence 1410, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1410
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 7
US-10-296-734-1410

Alignment Scores:
Pred. No.: 3.61 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-296-734-1410 (1-30)

QY 318 GAGTTCTACTGCGCATGCTTTCCGGAGACCCATGAGAGAGAGCTGCGCCGCGAGAC 377
Db 1 GuphetyLeuAlaMetProPheAlaThrProMetGluAlaGluLeuAlaArgSer 20

QY 378 CTGGCCAGAGATGCCCGACCGCTCCCGTG 407
Db 21 LeuAlaGlnAspAlaProProLeuProVal 30

RESULT 7
US-10-296-734-1412
; Sequence 1412, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1412
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 8
US-10-296-734-1412

Alignment Scores:
Pred. No.: 3.61 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-296-734-1412 (1-30)

QY 363 CTGGCCGCGAGAGCTTGCCCGAGATGCCCGACCGCTTCCGTCGAGGAGGCTCTTG 422
Db 1 LeuAlaArgSerLeuAlaGlnAspAlaProProLeuProValProGlyValLeuLeu 20

QY 423 AAGGAGTTCAGTGTGTCCGGCAACATCTG 452
Db 21 LysGluPheThrValSerGlyAsnIleLeu 30

RESULT 8
US-10-296-734-1414
; Sequence 1414, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1414
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 9
US-10-296-734-1414

Alignment Scores:
Pred. No.: 3.61 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-296-734-1414 (1-30)

QY 408 CCAAGGGGTGCTTGTGAAGAGTTCAGTGTGCCGCAACATATGACTATCCGACTGACT 467
Db 1 ProGlyValLeuLeuLysGluPheThrValSerGlyAsnIleLeuThrIleArgLeuThr 20

QY 468 GCTGCAGACCAACCGCAACTGCACCTTCC 497
Db 21 AlaIaAspHisArgGlnLeuGlnLeuSer 30

RESULT 9
US-10-296-734-1416
; Sequence 1416, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1416
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 10

US-10-296-734-1416

Alignment Scores:

Pred. No.: 3.61 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-296-734-1416 (1-30)

QY 453 ACTATCCAGTCTGCTGCTGACAGCCGCAACTGACGCTCCATCAGTCTGCTGCTC 512

Db 1 ThrileatgletthrAlaAlaaphisarglnleuSerileSerCysleu 20

QY 513 CAGCAGCTTCCCTGTTGATGTGATCAG 542

Db 21 GlnGlnleuSerleuMetTrrilethr 30

RESULT 10

US-10-296-734-1418

Sequence 1418, Application US/10296734
Publication No. US20040054137A1

GENERAL INFORMATION:

APPLICANT: Thompson, Scott A

TITLE OF INVENTION: Synthetic molecules and uses therefor

FILE REFERENCE: Savine

CURRENT APPLICATION NUMBER: US/10/296,734

CURRENT FILING DATE: 2003-08-04

PRIOR APPLICATION NUMBER: AU PQ7761/00

NUMBER OF SEQ ID NOS: 2000-05-26

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1418

LENGTH: 30

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: NYSOLA segment 11

US-10-296-734-1418

Alignment Scores:

Pred. No.: 3.61 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-296-734-1418 (1-30)

QY 498 ATCAGCTCTGCTGCTGACAGCTTCCCTGTGATGTGATCAGCAGTCTTCTGCCC 557

Db 1 IleserSerCysleuGlnGlnleuSerleuMetTrrilethrGlnCysheleuro 20

QY 558 GTGTTTGGCTCAGCTTCCCTCAGGGCAG 587

Db 21 ValPheleuAlaGlnProProserGlyGln 30

RESULT 11

US-10-296-734-1424

Sequence 1424, Application US/10296734
Publication No. US20040054137A1

GENERAL INFORMATION:

APPLICANT: Thompson, Scott A

TITLE OF INVENTION: Synthetic molecules and uses therefor

FILE REFERENCE: Savine

CURRENT APPLICATION NUMBER: US/10/296,734

CURRENT FILING DATE: 2003-08-04

PRIOR APPLICATION NUMBER: AU PQ7761/00

PRIOR FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1507

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1424

LENGTH: 30

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: NYSOLb segment 2

US-10-296-734-1424

Alignment Scores:

Pred. No.: 3.61 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-296-734-1424 (1-30)

QY 133 CAGGGGCAATGCTGGCGGCGCCAGAGAGCGGGTGCACGCGGCGAGAGCTCCCGCG 192

Db 1 GlnGlnAlaMetleuAlaAlaGlnGlnArgValProArgAlaAlaGlnValProGly 20

QY 193 GCGCAGGGGCGAGCAAGGGCTCGGGGCGG 222

Db 21 AlaGlnGlnGlnGlnGlyProArgGlyArg 30

RESULT 12

US-10-296-734-1426

Sequence 1426, Application US/10296734
Publication No. US20040054137A1

GENERAL INFORMATION:

APPLICANT: Thompson, Scott A

TITLE OF INVENTION: Synthetic molecules and uses therefor

FILE REFERENCE: Savine

CURRENT APPLICATION NUMBER: US/10/296,734

CURRENT FILING DATE: 2003-08-04

PRIOR APPLICATION NUMBER: AU PQ7761/00

NUMBER OF SEQ ID NOS: 2000-05-26

SOFTWARE: PatentIn version 3.2

SEQ ID NO 1426

LENGTH: 30

TYPE: PRT

ORGANISM: Artificial

FEATURE:

OTHER INFORMATION: NYSOLb segment 3

US-10-296-734-1426

Alignment Scores:

Pred. No.: 3.61 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-296-734-1426 (1-30)

QY 178 GCAGAGTCCCGGGGCGGCGGCGACAGAGGCTCGGGGCGGAGAGGCGGCGG 237

Db 1 AlaGlnValProGlnAlaGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 20

QY 238 GGGTCCGATGCGGCGGCGGCTTCAGGCG 267

Db 21 GlyValArgMetAlaAlaArgleuGlnGly 30

RESULT 13

US-10-296-734-1432

Sequence 1432, Application US/10296734

Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1432
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: LAG1 segment 2
US-10-296-734-1432

Alignment Scores:
Pred. No.: 3.61 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-296-734-1432 (1-30)

QY 93 GATGCTGATGCGCCGAGAGCGCCCTGGCATTCCTGATGCGCCGAGGCGGCAATGCTGCGGC 152
Db 1 AapAlaAepGlyProGlyGlyProGlyLeProAepGlyProGlyGlyAmaAlaGlyGly 20

QY 153 CGAGAGAGCGCGCGTGCACCGCGCGGCGGCA 182
Db 21 ProGlyGlyAlaGlyAlaThrGlyGlyArg 30

RESULT 14

US-10-364-614-16
; Sequence 16, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: Gnajatic, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 CIP
; CURRENT APPLICATION NUMBER: US/10/364,614
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-16

Alignment Scores:
Pred. No.: 3.61 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-364-614-16 (1-30)

QY 291 GCCAGGGGGCCGAGAGCGCCCTGCTTGAATTCCTGCGCATGCTTTGCGGACACCC 350
|||||

Db 1 AlaArgGlyProGlyUSeArgLeuLeuGlnUbeTyrLeuAlaMetProPheAlaThrPro 20
QY 351 ATGAGAGCAGACTGCGCCGAGAGCGCTG 380
Db 21 MetGlyAlaGlnLeuAlaArgArgSerLeu 30

RESULT 15
US-10-117-937-254
; Sequence 254, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 254
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-254

Alignment Scores:
Pred. No.: 4.99 Length: 28
Score: 28.00 Matches: 28
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 15.56% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-254 (1-28)

QY 459 CGACTGACTGCTGAGACCAACCGCAACTGCGAGCTTCATCAGCTCCTGTCACGAG 518
Db 1 ArgLeuThrAlaAlaAepHisArgGlnLeuGlnLeuSerSerCysLeuGlnGln 20

QY 519 CTTTCCTGTTGATGTGATCAG 542
Db 21 LeuSerLeuLeuMetTrrpIleThr 28

RESULT 16
US-10-117-937-255
; Sequence 255, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602

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/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 255
/ LENGTH: 28
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-117-937-255

Alignment Scores:
Pred. No.: 4.99      Length: 28
Score: 28.00      Matches: 28
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 15.56%      Indels: 0
Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-255 (1-28)

Qy 501 AGCTCTGTCACAGACCTTCCCTGTGATGATGATCAGCAGTCTTCTGCGCGG 560
Db 1 SerserCysleuGlnGlnleuSerleuMetRpiIethrGlnCysPheleuProval 20
Qy 561 TTTTGGCTCAGCCCTCCCTCAGGG 584
Db 21 PheleuAlaGlnProSerGly 28

RESULT 17
US-10-164-121A-35
/ Sequence 35, Application US/10164121A
/ Publication No. US20030228308A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Yi
/ APPLICANT: Boon, Thierry
/ APPLICANT: Van der Bruggen, Pierre
/ TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereof
/ FILE REFERENCE: LUD-5771
/ CURRENT APPLICATION NUMBER: US/10/164,121A
/ CURRENT FILING DATE: 2002-08-26
/ NUMBER OF SEQ ID NOS: 36
/ SEQ ID NO 35
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: H. sapiens
/ FEATURE:
US-10-164-121A-35

Alignment Scores:
Pred. No.: 16.8      Length: 20
Score: 20.00      Matches: 20
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 11.11%      Indels: 0
Gaps: 0

US-10-023-182-1 (1-752) x US-10-164-121A-35 (1-20)

Qy 408 CCAGGGGCTTCTTAAGAGTTCAGTGTGTCGGCAACATCTGACTATCGAGTGA 467
Db 1 ProGlyValLeuLeuLysGlnPheThrValSerGlyAsnIleuThrIleArgLeuThr 20

RESULT 18
US-10-164-078A-34
/ Sequence 34, Application US/10164078A
/ Publication No. US20030228325A1
/ GENERAL INFORMATION:
/ APPLICANT: Bilsborough, Janine
/ APPLICANT: Schultz, Erwin
/ APPLICANT: Panichelli, Christophe
/ APPLICANT: Van der Bruggen, Pierre
/ APPLICANT: Boon, Thierry
/ TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B18 Molecules And Uses Thereof
/ FILE REFERENCE: LUD-5756
/ CURRENT APPLICATION NUMBER: US/10/164,078A
```

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/ CURRENT FILING DATE: 2002-06-05
/ NUMBER OF SEQ ID NOS: 35
/ SEQ ID NO 34
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: H. sapiens
/ FEATURE:
US-10-164-078A-34

Alignment Scores:
Pred. No.: 16.8      Length: 20
Score: 20.00      Matches: 20
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 11.11%      Indels: 0
Gaps: 0

US-10-023-182-1 (1-752) x US-10-164-078A-34 (1-20)

Qy 408 CCAGGGGCTTCTTAAGAGTTCAGTGTGTCGGCAACATCTGACTATCGAGTGA 467
Db 1 ProGlyValLeuLeuLysGlnPheThrValSerGlyAsnIleuThrIleArgLeuThr 20

RESULT 19
US-10-313-986-492
/ Sequence 492, Application US/10313986
/ Publication No. US20030236209A1
/ GENERAL INFORMATION:
/ APPLICANT: Foy, Teresa M.
/ APPLICANT: McNabb, Andria
/ APPLICANT: Watanabe, Yoshihiro
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Wang, Tongtong
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.455C19
/ CURRENT APPLICATION NUMBER: US/10/313,986
/ CURRENT FILING DATE: 2002-12-04
/ NUMBER OF SEQ ID NOS: 560
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 492
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-313-986-492

Alignment Scores:
Pred. No.: 16.8      Length: 20
Score: 20.00      Matches: 20
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match: 11.11%      Indels: 0
Gaps: 0

US-10-023-182-1 (1-752) x US-10-313-986-492 (1-20)

Qy 84 TCGACGGGCGCATGCTGATGCGCCAGAGCCCTCGCATTCCTGATGCGCCAGGGGCAAT 143
Db 1 SerThrGlyAspAlaAspGlyProGlyGlyProGlyIleProAspGlyProGlyGlyAsn 20

RESULT 20
US-10-313-986-493
/ Sequence 493, Application US/10313986
/ Publication No. US20030236209A1
/ GENERAL INFORMATION:
/ APPLICANT: Foy, Teresa M.
/ APPLICANT: McNabb, Andria
/ APPLICANT: Watanabe, Yoshihiro
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Wang, Tongtong
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.455C19
```

```

; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 493
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-493

Alignment Scores:
Pred. No.:      16.8      Length:      20
Score:          20.00     Matches:      20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    11.11%   Indels:      0
DB:             1       Gaps:        0

US-10-023-182-1 (1-752) x US-10-313-986-493 (1-20)

QY      114 CCTGGCATTCTGTATGCCCGAGGGGCAATGCTGGCGGCCAGAGAGGGGGTGCACG 173
Db      1 TPrGlyIleProAspIlyProGlyGlyAsnIaGlyGlyProGlyGlnuIaGlyIaIaThr 20

RESULT 21
US-10-313-986-494
; Sequence 494, Application US/10313986
; Publication No. US20030236209A1
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 494
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-494

Alignment Scores:
Pred. No.:      16.8      Length:      20
Score:          20.00     Matches:      20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    11.11%   Indels:      0
DB:             1       Gaps:        0

US-10-023-182-1 (1-752) x US-10-313-986-494 (1-20)

QY      324 TACCTCGCCATGCTTTCCGCAACCCATGAGAGAGAGCTGAGCCGCGAGAGCCTGGCC 383
Db      1 TyrlaAlaMetProPhehIaIaThrProMetGlnuIaGlnuIaIaIaIaIaIaIaIaIa 20

RESULT 22
US-10-313-986-495
; Sequence 495, Application US/10313986
; Publication No. US20030236209A1
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: AND DIAGNOSIS OF LUNG CANCER
```

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; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 495
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-495

Alignment Scores:
Pred. No.:      16.8      Length:      20
Score:          20.00     Matches:      20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    11.11%   Indels:      0
DB:             1       Gaps:        0

US-10-023-182-1 (1-752) x US-10-313-986-495 (1-20)

QY      534 TGATCAGCAGTGTCTGCTCCGCTGTTTGGCTCAGCCTCCCTCAGAGAGGCGC 593
Db      1 TPrIleThrGlnCySPhelauProValPheIuIaGlnIaProIaSerGlyGlnIaIaIa 20

RESULT 23
US-10-313-986-496
; Sequence 496, Application US/10313986
; Publication No. US20030236209A1
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 496
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-496

Alignment Scores:
Pred. No.:      16.8      Length:      20
Score:          20.00     Matches:      20
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match:    11.11%   Indels:      0
DB:             1       Gaps:        0

US-10-023-182-1 (1-752) x US-10-313-986-496 (1-20)

QY      174 GCGGCAAGGTTCCTCCGAGGGGCGAGAGGGCTCGGGGCGGAGAGGCGCC 233
Db      1 GlyIlyIaIaGlyProIaGlyIaIaGlyIaIaIaIaIaIaIaIaIaIaIaIaIaIaIa 20

RESULT 24
US-10-364-614-5
; Sequence 5, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elike
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: Gujatic, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 CIP
```

```
; CURRENT APPLICATION NUMBER: US/10/364,614
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-5

Alignment Scores:
Pred. No.:      22      Length:      18
Score:          18.00   Matches:      18
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match:    10.00%   Indels:      0
DB:             1      Gaps:          0

US-10-023-182-1 (1-752) x US-10-364-614-5 (1-18)

QY      306 AGCGCCTGCTTGTACCTGCGCATGCTTTCGCGACACCCATGGAACA 359
DB      1 SerArgLeuGluGluPheTyrLeuAlaMetProPheAlaThrProMetGluAla 18

RESULT 25
US-10-364-614-6
; Sequence 6, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 CIP
; CURRENT APPLICATION NUMBER: US/10/364,614
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-6

Alignment Scores:
Pred. No.:      22      Length:      18
Score:          18.00   Matches:      18
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match:    10.00%   Indels:      0
DB:             1      Gaps:          0

US-10-023-182-1 (1-752) x US-10-364-614-6 (1-18)

QY      324 TACCTGCGCATGCTTTCGCGACACCCATGGAAGAGAGCTGGCCGAGAGGC 377
DB      1 TyrLeuAlaMetProPheAlaThrProMetGluAlaGluLeuAlaArgArgSer 18

RESULT 26
US-10-364-614-7
; Sequence 7, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: GnJatic, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
```

```
; FILE REFERENCE: LUD 5726.1 CIP
; CURRENT APPLICATION NUMBER: US/10/364,614
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 7
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-7

Alignment Scores:
Pred. No.:      22      Length:      18
Score:          18.00   Matches:      18
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match:    10.00%   Indels:      0
DB:             1      Gaps:          0

US-10-023-182-1 (1-752) x US-10-364-614-7 (1-18)

QY      360 GAGCTGCGCCGACAGAGCTGCGCCAGAGATGCCACCGCTTCCCGCAGAGG 413
DB      1 GluLeuAlaArgArgSerLeuAlaGlnAspAlaProProLeuProValProGly 18

RESULT 27
US-10-164-121A-36
; Sequence 36, Application US/10164121A
; Publication No. US20030228308A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Boon, Thierry
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Traversari, Catia
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5771
; CURRENT APPLICATION NUMBER: US/10/164,121A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 36
; LENGTH: 18
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-164-121A-36

Alignment Scores:
Pred. No.:      22      Length:      18
Score:          18.00   Matches:      18
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match:    10.00%   Indels:      0
DB:             1      Gaps:          0

US-10-023-182-1 (1-752) x US-10-164-121A-36 (1-18)

QY      468 GCTGACAGCACCGCAACTGTCAGCTTCATCAGCTTCCTGTCACAGACGCTT 521
DB      1 AlaAlaPhePheSerGlnLeuGlnLeuSerIleSerSerCysLeuGlnGlnLeu 18

RESULT 28
US-10-164-078A-35
; Sequence 35, Application US/10164078A
; Publication No. US20030228325A1
; GENERAL INFORMATION:
; APPLICANT: Bilborough, Janine
; APPLICANT: Schultze, Brian
; APPLICANT: Panichelli, Christophe
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B*8 Molecules And Uses Thereof
```

FILE REFERENCE: LUD-5756
CURRENT APPLICATION NUMBER: US/10/164,078A
CURRENT FILING DATE: 2002-06-05
NUMBER OF SEQ ID NOS: 35
SEQ ID NO 35
LENGTH: 18
TYPE: PRT
ORGANISM: H. sapiens
FEATURE:
US-10-164-078A-35

Alignment Scores:
Pred. No.: 22 Length: 18
Score: 18.00 Matches: 18
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 10.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-164-078A-35 (1-18)

OY 468 GGTGAGACCACTGAGCTCTCCATCAGCTCTCTCCAGAGCTT 521
Db 1 AAlaAlaSPHlArgGlnLeuGlnLeuSerIleSerCysLeuGlnLeu 18

RESULT 29
US-09-751-798-4
Sequence 4, Application US/09751798
Patent No. US20020010321A1

GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES: 8

CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA

ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM

OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798

FILING DATE:
Prior Application Data:
APPLICATION NUMBER: 09/062,422

FILING DATE:
Prior Application Data:
APPLICATION NUMBER: 08/725,182

FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020010321A1man D.

REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5598

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear

US-09-751-798-4

Alignment Scores:
Pred. No.: 50.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-751-798-4 (1-11)

OY 522 TCCCTGTGATGTGATCAGCAGTCTTCTG 554
Db 1 SerLeuLeuMetTrpIleThrGlnCysPheLeu 11

RESULT 30
US-09-766-889A-50
Sequence 50, Application US/09766889A
Patent No. US20020164654A1

GENERAL INFORMATION:
APPLICANT: Luiten, Rosalie
APPLICANT: Boon-Falleur, Thierry
APPLICANT: van der Bruggen, Pierre
APPLICANT: Stroobant, Vincent
APPLICANT: Demotte, Nathalie
APPLICANT: Schuitz, Erwin
TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
FILE REFERENCE: L0461/7104
CURRENT APPLICATION NUMBER: US/09/766,889A
CURRENT FILING DATE: 2001-01-19
Prior Application Number: US 60/177,242
Prior Filing Date: 2000-01-20
Prior Application Number: US 60/243,212
Prior Filing Date: 2000-10-25
NUMBER OF SEQ ID NOS: 59

SOFTWARE: PastSeq for Windows Version 3.0
SEQ ID NO 50
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-09-766-889A-50

Alignment Scores:
Pred. No.: 50.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-766-889A-50 (1-11)

OY 522 TCCCTGTGATGTGATCAGCAGTCTTCTG 554
Db 1 SerLeuLeuMetTrpIleThrGlnCysPheLeu 11

RESULT 31

US-10-218-095-45
Sequence 45, Application US/10218095
Publication No. US20040033541A1

GENERAL INFORMATION:
APPLICANT: Zhang, Yi
APPLICANT: Stroobant, Vincent

APPLICANT: Russo, Vincenzo
APPLICANT: Boon-Falleur, Thierry

APPLICANT: van der Bruggen, Pierre
TITLE OF INVENTION: MAGE-A4 ANTIGENIC PEPTIDES AND USES THEREOF

FILE REFERENCE: L00461/70137
CURRENT APPLICATION NUMBER: US/10/218,095

CURRENT FILING DATE: 2002-08-13

NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.1

SEQ ID NO 45
LENGTH: 11

TYPE: PRT
ORGANISM: Homo sapiens
US-10-218-095-45

Alignment Scores:
Pred. No.: 50.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-218-095-45 (1-11)

QY 522 TCCTGTGATGATCAGCAGGCTTTCTG 554
Db 1 SerineuemetriplietrhGincyphelen 11

RESULT 32
US-10-023-182-4
Sequence 4, Application US/10023182
Publication No. US20020164665A1

GENERAL INFORMATION:
APPLICANT: Scockert, Elisabeth; Jager, Elke;
Chen, Yao-teeng; Scanlan, Matthew;
Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
Associated Proteins, Uses Thereof,
Truncated Forms of NY-ESO-1, and HLA
Binding Peptides Derived Therefrom

NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage

COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/023,182
FILING DATE: 17-Dec-2001

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/751,798
FILING DATE: December 29, 2000
APPLICATION NUMBER: 09/062,422
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996

ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020164665A1man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-023-182-4

Alignment Scores:
Pred. No.: 50.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-023-182-4 (1-11)

QY 522 TCCTGTGATGATCAGCAGGCTTTCTG 554
Db 1 SerineuemetriplietrhGincyphelen 11

RESULT 33
US-10-161-097-33
Sequence 33, Application US/10161097
Publication No. US20030096404A1

GENERAL INFORMATION:
APPLICANT: ROSENZWEIG, Michael
APPLICANT: PYKEET, Mark J.
APPLICANT: SCADDEN, David T.
APPLICANT: POZNANSKY, Mark C.
TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
FILE REFERENCE: C1005/7012/KA/ERG

CURRENT APPLICATION NUMBER: US/10/161,097
CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US/09/574,749
PRIOR FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: US 60/107,972
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: PCT/US99/26795
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: US 09/524,749
PRIOR FILING DATE: 2000-05-18

NUMBER OF SEQ ID NOS: 58
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Homo Sapiens source
US-10-161-097-33

Alignment Scores:
Pred. No.: 50.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-161-097-33 (1-11)

QY 522 TCCTGTGATGATCAGCAGGCTTTCTG 554
Db 1 SerineuemetriplietrhGincyphelen 11

RESULT 34
US-10-170-832-79
Sequence 79, Application US/10170832
Publication No. US2003017092A1

GENERAL INFORMATION:
APPLICANT: Chaux, Pascal
APPLICANT: Vantomme, Valrie
APPLICANT: Strobant, Vincent
APPLICANT: Boon-Falleur, Thierry
APPLICANT: van der Bruggen, Pierre
APPLICANT: Thielemans, Kris
APPLICANT: Cortals, Jorgen
TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
FILE REFERENCE: L0461/7052
CURRENT APPLICATION NUMBER: US/10/170,832
CURRENT FILING DATE: 2002-06-12
PRIOR APPLICATION NUMBER: US/09/166,448

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/ PRIOR FILING DATE: 1998-10-05
/ NUMBER OF SEQ ID NOS: 81
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 79
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-170-832-79

Alignment Scores:
Pred. No.: 50.1      Length: 11
Score: 11.00        Matches: 11
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 6.11%      Indels: 0
DB: 1                Gaps: 0

US-10-023-182-1 (1-752) x US-10-170-832-79 (1-11)

Qy 522 TCCTGTGATGTGATCAGCAGTGTCTTG 554
Db 1 SerleuMetTrrpIleThrGlnCysPheIeu 11

RESULT 35
US-10-364-614-9
/ Sequence 9, Application US/10364614
/ Publication No. US20030175250A1
/ GENERAL INFORMATION:
/ APPLICANT: JAGER, Elke
/ APPLICANT: KNUTH, Alexander
/ APPLICANT: OLD, Lloyd
/ APPLICANT: Gnjaic, Sacha
/ TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
/ FILE REFERENCE: LUD 5726.1 CIP
/ CURRENT APPLICATION NUMBER: US/10/364,614
/ PRIOR FILING DATE: 2003-02-24
/ PRIOR APPLICATION NUMBER: US 60/355,828
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 9
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-364-614-9

Alignment Scores:
Pred. No.: 50.1      Length: 11
Score: 11.00        Matches: 11
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 6.11%      Indels: 0
DB: 1                Gaps: 0

US-10-023-182-1 (1-752) x US-10-364-614-9 (1-11)

Qy 522 TCCTGTGATGTGATCAGCAGTGTCTTG 554
Db 1 SerleuMetTrrpIleThrGlnCysPheIeu 11

RESULT 36
US-10-177-277-130
/ Sequence 130, Application US/10177277
/ Publication No. US20030185844A1
/ GENERAL INFORMATION:
/ APPLICANT: Tureci, Ozlem
/ APPLICANT: Sahin, Ugur
/ APPLICANT: Pfreundschuh, Michael
/ APPLICANT: Ramensee, Hans Georg
/ APPLICANT: Stevanovic, Stefan
/ TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determining Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
/ TITLE OF INVENTION: Gene, and Uses Thereof
```

```
/ FILE REFERENCE: LUD 5556.1
/ CURRENT APPLICATION NUMBER: US/10/177,277
/ CURRENT FILING DATE: 2002-06-21
/ PRIOR APPLICATION NUMBER: US/09/344,040
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: US 09/105,839
/ PRIOR FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: US 08/851,130
/ PRIOR FILING DATE: 1997-05-05
/ NUMBER OF SEQ ID NOS: 132
/ SEQ ID NO 130
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-177-277-130

Alignment Scores:
Pred. No.: 50.1      Length: 11
Score: 11.00        Matches: 11
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 6.11%      Indels: 0
DB: 1                Gaps: 0

US-10-023-182-1 (1-752) x US-10-177-277-130 (1-11)

Qy 522 TCCTGTGATGTGATCAGCAGTGTCTTG 554
Db 1 SerleuMetTrrpIleThrGlnCysPheIeu 11

RESULT 37
US-10-164-121A-29
/ Sequence 29, Application US/10164121A
/ Publication No. US20030228308A1
/ GENERAL INFORMATION:
/ APPLICANT: Zhang, Yi
/ APPLICANT: Boon, Thierry
/ APPLICANT: Van der Bruggen, Pierre
/ APPLICANT: Traversari, Catra
/ TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereof
/ FILE REFERENCE: LUD-5771
/ CURRENT APPLICATION NUMBER: US/10/164,121A
/ CURRENT FILING DATE: 2002-08-26
/ NUMBER OF SEQ ID NOS: 36
/ SEQ ID NO 29
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: H. sapiens
US-10-164-121A-29

Alignment Scores:
Pred. No.: 50.1      Length: 11
Score: 11.00        Matches: 11
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 6.11%      Indels: 0
DB: 1                Gaps: 0

US-10-023-182-1 (1-752) x US-10-164-121A-29 (1-11)

Qy 522 TCCTGTGATGTGATCAGCAGTGTCTTG 554
Db 1 SerleuMetTrrpIleThrGlnCysPheIeu 11

RESULT 38
US-10-164-078A-28
/ Sequence 28, Application US/10164078A
/ Publication No. US20030228325A1
/ GENERAL INFORMATION:
/ APPLICANT: Bilbrough, Janine
/ APPLICANT: Schultz, Erwin
/ APPLICANT: Panichelli, Christophe
```



```
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B*8 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5756
; CURRENT APPLICATION NUMBER: US/10/164,078A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 28
; LENGTH: 11
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-078A-28

Alignment Scores:
Pred. No.: 50.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-164-078A-28 (1-11)
QY 522 TCCTGTGATGTGATCAGCAGTCTTCTG 554
DB 1 SerleuMettrpIleThrGlnCysPheLeu 11

RESULT 39
US-10-447-161-36
; Sequence 36, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 36
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-36

Alignment Scores:
Pred. No.: 50.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-447-161-36 (1-11)
QY 522 TCCTGTGATGTGATCAGCAGTCTTCTG 554
DB 1 SerleuMettrpIleThrGlnCysPheLeu 11

RESULT 40
US-10-447-161-81
; Sequence 81, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
```

```
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
US-10-447-161-81

Alignment Scores:
Pred. No.: 50.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-447-161-81 (1-11)
QY 94 ATGCTGATGGCCAGAGGCCCTGGCATTCCTG 126
DB 1 MetleuMetalaGlnGlnAlaLeuAlaPheLeu 11

RESULT 41
US-10-447-161-82
; Sequence 82, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-82

Alignment Scores:
Pred. No.: 50.1 Length: 11
Score: 11.00 Matches: 11
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 6.11% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-447-161-82 (1-11)
QY 94 ATGCTGATGGCCAGAGGCCCTGGCATTCCTG 126
DB 1 MetleuMetalaGlnGlnAlaLeuAlaPheLeu 11

RESULT 42
US-10-706-475-1
; Sequence 1, Application US/10706475
; Publication No. US20040077548A1
; GENERAL INFORMATION:
; APPLICANT: Cerundolo, Vincenzo
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629.1
; CURRENT APPLICATION NUMBER: US/10/706,475
; CURRENT FILING DATE: 2003-11-11
```

PRIOR APPLICATION NUMBER: US/09/514,036E
 PRIOR FILING DATE: 2000-02-25
 PRIOR APPLICATION NUMBER: US 09/440,621
 PRIOR FILING DATE: 1999-11-15
 PRIOR APPLICATION NUMBER: US 09/165,546
 PRIOR FILING DATE: 1998-10-02
 PRIOR APPLICATION NUMBER: US 09/062,422
 PRIOR FILING DATE: 1998-04-17
 PRIOR APPLICATION NUMBER: US 08/725,162
 PRIOR FILING DATE: 1996-10-03
 NUMBER OF SEQ ID NOS: 18
 SEQ ID NO 1
 TYPE: PRT
 LENGTH: 11
 ORGANISM: Homo sapiens
 US-10-706-475-1
 Alignment Scores:
 Pred. No.: 50.1
 Score: 11.00
 Matches: 11
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 6.11%
 Indels: 0
 Gaps: 0
 DB: 1
 US-10-023-182-1 (1-752) x US-10-706-475-1 (1-11)
 QY 522 TCCCTGTGATGGATCAGCAGTGTCTTCTG 554
 Db 1 Serleuemetrlprietnrglncysphelu 11
 RESULT 43
 US-10-415-841A-54
 Sequence 54, Application US/10415841A
 Publication No. US20040131598A1
 GENERAL INFORMATION:
 APPLICANT: Tafuro, Sabrina
 APPLICANT: Meyer, Ute-Christiane
 APPLICANT: McMichael, Andrew James
 APPLICANT: Bell, John Irving
 APPLICANT: Layton, Guy
 APPLICANT: Hunter, Michael
 TITLE OF INVENTION: Cancer Therapy
 FILE REFERENCE: 3547,1001-000
 CURRENT APPLICATION NUMBER: US/10/415,841A
 CURRENT FILING DATE: 2004-01-21
 PRIOR APPLICATION NUMBER: PCT/GB01/04844
 PRIOR FILING DATE: 2001-11-01
 NUMBER OF SEQ ID NOS: 57
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 54
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-415-841A-54
 Alignment Scores:
 Pred. No.: 50.1
 Score: 11.00
 Matches: 11
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 6.11%
 Indels: 0
 Gaps: 0
 DB: 1
 US-10-023-182-1 (1-752) x US-10-415-841A-54 (1-11)
 QY 94 ATGCTGATGGCCGAGAGGCCCTGGCATTTCCTG 126
 Db 1 MetleuetaclaginciuatleuAlaphelu 11
 RESULT 44
 US-10-296-734-1400
 Sequence 1400, Application US/10296734
 Publication No. US20040054137A1
 GENERAL INFORMATION:
 APPLICANT: Thompson, Scott A
 APPLICANT: Ramshaw, Ian A
 TITLE OF INVENTION: Synthetic molecules and uses therefor
 FILE REFERENCE: Savine
 CURRENT APPLICATION NUMBER: US/10/296,734
 CURRENT FILING DATE: 2003-08-04
 PRIOR APPLICATION NUMBER: AU P07761/00
 PRIOR FILING DATE: 2000-05-26
 NUMBER OF SEQ ID NOS: 1507
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 1400
 LENGTH: 30
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: NYSOIA segment 2
 US-10-296-734-1400
 Alignment Scores:
 Pred. No.: 72.6
 Score: 11.00
 Matches: 30
 Percent Similarity: 44.00%
 Best Local Similarity: 44.00%
 Query Match: 6.18%
 Indels: 14
 Gaps: 0
 DB: 1
 US-10-023-182-1 (1-752) x US-10-296-734-1400 (1-30)
 QY 187 GGACCTGCGCGCGCGGAGCAGCCGCTCTCGTGGGCGCGACGATGCCCCCTGGAGCCA 128
 Db 4 GlyProgllylProgllylIleProaspGlyProgllylYasnAlaGlylProgllylGlu 23
 QY 127 TCAGGAATGCCAGGG 113
 Db 24 AlaGlyAlaThrGly 28
 RESULT 45
 US-10-296-734-1404
 Sequence 1404, Application US/10296734
 Publication No. US20040054137A1
 GENERAL INFORMATION:
 APPLICANT: Thompson, Scott A
 APPLICANT: Ramshaw, Ian A
 TITLE OF INVENTION: Synthetic molecules and uses therefor
 FILE REFERENCE: Savine
 CURRENT APPLICATION NUMBER: US/10/296,734
 CURRENT FILING DATE: 2003-08-04
 PRIOR APPLICATION NUMBER: AU P07761/00
 PRIOR FILING DATE: 2000-05-26
 NUMBER OF SEQ ID NOS: 1507
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 1404
 LENGTH: 30
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: NYSOIA segment 4
 US-10-296-734-1404
 Alignment Scores:
 Pred. No.: 72.6
 Score: 11.00
 Matches: 30
 Percent Similarity: 44.00%
 Best Local Similarity: 44.00%
 Query Match: 6.18%
 Indels: 14
 Gaps: 0
 DB: 1
 US-10-023-182-1 (1-752) x US-10-296-734-1404 (1-30)
 QY 274 CCATTACGCTTGAAGCGCGCGCCCATGCGAGCCCGCGGCGGCGCTCTCTCCCGGCGCC 215
 Db 1 MetleuetaclaginciuatleuAlaphelu 11

Db 2 ProArglyAlaGlyAlaAlaArgAlaSerGlyProGlyGlyAlaProArgGlyPro 21
OY 214 GAGGCCCTTGCTGCC 200
Db 22 HisGlyGlyAlaAla 26

RESULT 46
US-10-296-734-1432
; Sequence 1432, Application US//10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; NUMBER OF SEQ ID NOS: 2000-05-26
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1432
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: LAGE1 segment 2
US-10-296-734-1432

Alignment Scores:
Pred. No.: 72.6 Length: 30
Score: 11.00 Matches: 11
Percent Similarity: 44.00% Conservative: 0
Best Local Similarity: 44.00% Mismatches: 14
Query Match: 6.18% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-296-734-1432 (1-30)

OY 187 GGACCTCGCCGCCGCCGCGCCCTCTCTGCGCCGACGATTCGCCCTTGAGCCA 128
Db 4 GlyProGlyGlyProGlyAlaProAspGlyProGlyGlyAsnAlaGlyGlyProGlyGlu 23

OY 127 TCAGGAATGCCAGG 113
Db 24 AlaGlyAlaThrGly 28

RESULT 47
US-09-572-404B-12
; Sequence 12, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 12
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in CTAG at 58-67 and may interact with Sequence
US-09-572-404B-12

Alignment Scores:
Pred. No.: 55 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 0 Gaps: 0

Query Match: 5.56% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-572-404B-12 (1-10)

OY 225 GAGGCGCCCGCGCGGTCGCGATGCGCGC 254
Db 1 GlyGlyAlaProArgGlyProHisGlyGly 10

RESULT 48
US-09-572-404B-3740
; Sequence 3740, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 3740
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in CTAG at 44-53 and may interact with Sequence :
US-09-572-404B-3740

Alignment Scores:
Pred. No.: 55 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-572-404B-3740 (1-10)

OY 183 GGTCCCGCGCGCGGCGAGCGAGCGGCC 212
Db 1 GlyProArglyAlaGlyAlaAlaArgAla 10

RESULT 49
US-09-572-404B-3741
; Sequence 3741, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProPatent version 1.0
; SEQ ID NO 3741
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in CTAG at 44-53 and may interact with Sequence :
US-09-572-404B-3741

Alignment Scores:
Pred. No.: 55 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56% Indels: 0
DB: 1 Gaps: 0


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; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 129
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039-129

Alignment Scores:
Pred. No.: 55          Length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039-129 (1-10)

QY 537 ATCAGCAGTGTCTTCGCGCTTTTG 566
Db 1 11etnrgInCyephelenuProvalphelu 10

RESULT 54
US-10-364-614-12
; Sequence 12, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: Gnjaetic, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 C1P
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-12

Alignment Scores:
Pred. No.: 55          Length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-364-614-12 (1-10)

QY 342 GCGACACCCATGAGCAGAGCTGCGCCGC 371
Db 1 1A1atnrrPrometGluA1agluDeuA1aarg 10

RESULT 55
US-10-364-614-17
; Sequence 17, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: Gnjaetic, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 C1P
; CURRENT APPLICATION NUMBER: US/10/364,614
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```
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-17

Alignment Scores:
Pred. No.: 55          Length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-364-614-17 (1-10)

QY 330 GCCATGCTTTGCGACACCCATGGAAGCA 359
Db 1 1AlametProPheal1atnrrPrometGluA1a 10

RESULT 56
US-10-177-277-126
; Sequence 126, Application US/10177277
; Publication No. US20030185844A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfeundschnuh, Michael
; APPLICANT: Ramenese, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determini
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene at
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 126
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-126

Alignment Scores:
Pred. No.: 55          Length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-177-277-126 (1-10)

QY 168 GCCACGCGCGGCGACAGAGTCCCGCGCGCA 197
Db 1 1A1atnrrGlyG1yArgG1yProArgG1yA1a 10

RESULT 57
US-10-177-277-127
; Sequence 127, Application US/10177277
; Publication No. US20030185844A1
; GENERAL INFORMATION:
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DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-177-277-128 (1-10)
Qy 363 CTGGCCGCGAGAGCCTTGGCCGAGATGCC 392
      ||||||||||||||||||||||||||||
Db 1 LeuAlaArgSerLeuAlaGlnAla 10

RESULT 59
US-10-177-277-129
; Sequence 129, Application US/10177277
; Publication No. US20030185844A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determinin
; TITLE OF INVENTION: Expression of an Ssx Gene, Peptides Derived From Said Ssx Gene ar
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 129
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-129

Alignment Scores:
Pred. No.: 55 Length: 10
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-177-277-129 (1-10)
Qy 537 ATCAGCAGTGCTTCTGCGCGTGTGTTT 566
      ||||||||||||||||||||||||||||
Db 1 IlethrgInCyphelauProvalPheleu 10

RESULT 60
US-10-117-937-171
; Sequence 171, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMO NO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Zhiping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPIPTO SEQUENCES
; FILE REFERENCE: CTILIM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0

```

```
; SEQ ID NO 171
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-171

Alignment Scores:
Pred. No.: 55          Length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-171 (1-10)

Cy 297 GGGCCGAGAGCCGCTTGAGTTCTAC 326
Db 1 GlyProGluSerArgLeuLeuGluPheTyr 10

RESULT 61
US-10-117-937-175
; Sequence 175, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT FILING DATE: 2002-04-04
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 175
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-175

Alignment Scores:
Pred. No.: 55          Length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-175 (1-10)

Cy 312 CTGCTTGAGTTCTACCTGCGCATGCTTTC 341
Db 1 LeuLeuGluPheTyrLeuAlaMetProPhe 10

RESULT 62
US-10-117-937-176
; Sequence 176, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
```

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; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 176
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-176

Cy 330 GCCATGCTTGCGGACACCGCATGAGACA 359
Db 1 AlaMetProPheAlaThrProMetGluAla 10

RESULT 63
US-10-117-937-179
; Sequence 179, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT FILING DATE: 2002-04-04
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 179
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-179

Alignment Scores:
Pred. No.: 55          Length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.56%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-179 (1-10)

Cy 393 CCACCGCTTGCGGACGAGGGGCTTCTG 422
Db 1 ProProLeuProValProGlyValLeuLeu 10
```

```
RESULT 64
US-10-117-937-181
; Sequence 181, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 181
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-181

Alignment Scores:
Pred. No.: 55          length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-181 (1-10)
QY 360 GAGCTGCGCCGAGGAGCCTGCGCCGAGAT 389
Db 1 GtLeuAlArGArGSerLeuAlaGlnAep 10

RESULT 65
US-10-117-937-183
; Sequence 183, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 183
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-183

Alignment Scores:
Pred. No.: 55          length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%      Indels: 0
DB: 1                  Gaps: 0
```

```
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-183 (1-10)
QY 402 CCCGTGCCAGGGGTCTTCTGAAGAGTTC 431
Db 1 ProValProGlyValLeuLeuValGluPhe 10

RESULT 66
US-10-117-937-186
; Sequence 186, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 186
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-186

Alignment Scores:
Pred. No.: 55          length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-186 (1-10)
QY 429 TTCACGTGTCCGCGACATCTGACTATTC 458
Db 1 PheThrValSerGlyAsnIleLeuThrIle 10

RESULT 67
US-10-117-937-188
; Sequence 188, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
```



```
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 188
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-188

Alignment Scores:
Pred. No.: 55          Length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-188 (1-10)
QY 414 GTGCTTGAAGAGATTCTGTCGCGC 443
Db 1 ValLeuLeuYsGluPheThrValSerCly 10

RESULT 68
US-10-117-937-191
; Sequence 191, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOP SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 191
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-191

Alignment Scores:
Pred. No.: 55          Length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-191 (1-10)
QY 402 CCGGTCGAGGGGCTCTGAAGAGTTC 431
Db 1 ProValIProGlyValLeuLeuYsGluPhe 10

RESULT 69
US-10-117-937-194
; Sequence 194, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
```

```
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOP SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 194
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-194

Alignment Scores:
Pred. No.: 55          Length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-194 (1-10)
QY 492 CTCCTCAGCAGCTCTCTCAGCAGCTT 521
Db 1 LeuSerIleSerSerCysLeuGlnGlnLeu 10

RESULT 70
US-10-117-937-195
; Sequence 195, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOP SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 195
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-195

Alignment Scores:
Pred. No.: 55          Length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-195 (1-10)
QY 465 ACTGCTGAGACGACCGCAACTGACCTC 494
Db 1
```

```
Db          1 ThrAlaAlaAspHisArgGlnLeuGlnLeu 10
RESULT 71
US-10-117-937-201
; Sequence 201, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhihong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 201
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-201

Alignment Scores:
Pred. No.: 55          Length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%          Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-201 (1-10)
QY          501 AGTCCTGCTGCAGCAGCTTCCCGTTG 530
Db          1 SerSerCysLeuGlnIleuSerLeuLeu 10

RESULT 72
US-10-117-937-203
; Sequence 203, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhihong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 203
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-203

Alignment Scores:
Pred. No.: 55          Length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%          Indels: 0
DB: 1                  Gaps: 0
```

```
Pred. No.: 55          Length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%          Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-203 (1-10)
QY          537 ATCAGCAGTGTCTTCGCGCGTGTGTTTG 566
Db          1 IleHnGlnCysPheLeuProValPheLeu 10

RESULT 73
US-10-117-937-357
; Sequence 357, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhihong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 357
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-357

Alignment Scores:
Pred. No.: 55          Length: 10
Score: 10.00          Matches: 10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%          Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-357 (1-10)
QY          240 GATCGCATGGCGGCGCGCTTCAGGGCTG 269
Db          1 GlyProHisGlyGlyAlaHisSerGlyLeu 10

RESULT 74
US-10-117-937-358
; Sequence 358, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhihong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
```

```
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 358
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-358

Alignment Scores:
Pred. No.: 55      Length: 10
Score: 10.00      Matches: 10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%  Indels: 0
DB: 1      Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-358 (1-10)
QY 231 GCGCGGGGCTCGCATGGCGGCGGCT 260
Db 1 AlaProArgGlyProHisGlyAlaAla 10

RESULT 75
US-10-447-161-39
; Sequence 39, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; PRIOR FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-39

Alignment Scores:
Pred. No.: 55      Length: 10
Score: 10.00      Matches: 10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%  Indels: 0
DB: 1      Gaps: 0

US-10-023-182-1 (1-752) x US-10-447-161-39 (1-10)
QY 210 GCCTCGGGGCGGAGAGCGGCCCGCGG 239
Db 1 AlaSerGlyProGlyGlyAlaProArg 10

RESULT 76
US-10-447-161-139
; Sequence 139, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; PRIOR FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 139
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-139

Alignment Scores:
Pred. No.: 55      Length: 10
Score: 10.00      Matches: 10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%  Indels: 0
DB: 1      Gaps: 0

US-10-023-182-1 (1-752) x US-10-447-161-139 (1-10)
QY 414 GTGCTTGAAGAGTTCACTGTGCGGC 443
Db 1 ValIleuLeuYsGIuPheHnValSerGly 10

RESULT 77
US-10-706-475-11
; Sequence 11, Application US/10706475
; Publication No. US20040077548A1
; GENERAL INFORMATION:
; APPLICANT: Cerundolo, Vincenzo
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629.1
; CURRENT APPLICATION NUMBER: US/10/706,475
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: US/09/514,036E
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 09/440,621
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 09/165,546
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: US 09/062,422
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 08/725,162
; PRIOR FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 11
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-475-11

Alignment Scores:
Pred. No.: 55      Length: 10
Score: 10.00      Matches: 10
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.56%  Indels: 0
DB: 1      Gaps: 0

US-10-023-182-1 (1-752) x US-10-706-475-11 (1-10)
QY 522 TCCCTGTGATGTGATCAGCATGCTTT 551
Db 1 SerIleuMetTrpIleHnGlnCysPhe 10

RESULT 78
US-10-415-841A-52
; Sequence 52, Application US/10415841A
; Publication No. US20040131598A1
; GENERAL INFORMATION:
; APPLICANT: Tafuro, Sabrina
; APPLICANT: Meter, Ute-Christiane
; APPLICANT: McMichael, Andrew James
; APPLICANT: Bell, John Irving
```

```

; APPLICANT: Layton, Michael
; TITLE OF INVENTION: Cancer Therapy
; FILE REFERENCE: 3547.1001-000
; CURRENT APPLICATION NUMBER: US/10/415, 841A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: PCT/GB01/04844
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-841A-52
Alignment Scores:
Pred. No.: 55
Score: 10.00
Length: 10
Percent Similarity: 100.00%
Matches: 10
Best Local Similarity: 100.00%
Conservative: 0
Query Match: 5.56%
Indels: 0
Gaps: 0
DB: 1
US-10-023-182-1 (1-752) x US-10-415-841A-52 (1-10)
CY 210 GCCTGGGGCCGGAGAGAGCGCCCGCG 239
Db 1 AAlserglyProglyglyAlaProArg 10
RESULT 79
US-10-415-841A-53
; Sequence 53, Application US/10415841A
; Publication No. US20040131598A1
; GENERAL INFORMATION:
; APPLICANT: Tafuro, Sabrina
; APPLICANT: Meier, Ute-Christiane
; APPLICANT: McMichael, Andrew James
; APPLICANT: Bell, John Irving
; APPLICANT: Layton, Michael
; TITLE OF INVENTION: Cancer Therapy
; FILE REFERENCE: 3547.1001-000
; CURRENT APPLICATION NUMBER: US/10/415, 841A
; CURRENT FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: PCT/GB01/04844
; PRIOR FILING DATE: 2001-11-01
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-415-841A-53
Alignment Scores:
Pred. No.: 55
Score: 10.00
Length: 10
Percent Similarity: 100.00%
Matches: 10
Best Local Similarity: 100.00%
Conservative: 0
Query Match: 5.56%
Indels: 0
Gaps: 0
DB: 1
US-10-023-182-1 (1-752) x US-10-415-841A-53 (1-10)
CY 145 CTGGCGGCGGAGAGAGCGGCGCCACGG 174
Db 1 LeuAlaAlaGInGluArgArgValProArg 10
RESULT 80
US-10-296-734-1406
Sequence 1406, Application US/10296734
Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296, 734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1406
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 5
US-10-296-734-1406
Alignment Scores:
Pred. No.: 75.8
Score: 10.00
Length: 30
Percent Similarity: 33.33%
Matches: 10
Best Local Similarity: 33.33%
Conservative: 0
Query Match: 5.62%
Indels: 20
Gaps: 0
DB: 1
US-10-023-182-1 (1-752) x US-10-296-734-1406 (1-30)
CY 349 GGTGCGGAAGGACATCGGAGCTCTTCATAGGTGTCGGAAGGC 335
Db 1 GlyAlaProArgGlyProHieGlyAlaAlaSerGlyLeuAngGlyCySvArgCyS 20
CY 334 ATGGCGAGTAACTCAAGCGGCGCTC 305
Db 21 GlyAlaArgGlyProGluSerArgLeuLeu 30
RESULT 81
US-10-296-734-1408
; Sequence 1408, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296, 734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU P07761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1408
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 6
US-10-296-734-1408
Alignment Scores:
Pred. No.: 75.8
Score: 10.00
Length: 30
Percent Similarity: 33.33%
Matches: 10
Best Local Similarity: 33.33%
Conservative: 0
Query Match: 5.62%
Indels: 20
Gaps: 0
DB: 1
US-10-023-182-1 (1-752) x US-10-296-734-1408 (1-30)
CY 349 GGTGCGGAAGGACATCGGAGCTCTTCATAGGTGTCGGAAGGC 290
Db 1 GlyCySvArgCySgGlyAlaArgGlyProGluSerArgLeuGluGluPheTyrlleuAla 20

```

Qy 289 CCGCATCTGCAGCATTCATCCAGCCCTGAA 260
Db 21 MetProhealathrPromeGluAlaGlu 30

RESULT 82
US-10-364-614-16
Sequence 16, Application US/10364614
Publication No. US20030175250A1
GENERAL INFORMATION:
APPLICANT: JAGER, Elke
APPLICANT: KNUTH, Alexander
APPLICANT: OLD, Lloyd
APPLICANT: Gnjatic, Sacha
TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
FILE REFERENCE: LUD 5726.1 CIP
CURRENT APPLICATION NUMBER: US/10/364,614
PRIOR FILING DATE: 2003-02-24
PRIOR APPLICATION NUMBER: US 60/355,828
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PatentIn version 3.2
SEQ ID NO 16
LENGTH: 30
TYPE: PRT
ORGANISM: Homo sapiens
US-10-364-614-16

Alignment Scores:
Pred. No.: 75.8 Length: 30
Score: 10.00 Matches: 10
Percent Similarity: 38.46% Conservative: 0
Best Local Similarity: 38.46% Mismatches: 16
Query Match: 5.62% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-364-614-16 (1-30)

Qy 331 GCGAGTGAAGACTCAAGCAGCGGCTCTCCGCGCCCTGCGCCGATCTGCAGATCCA 272
Db 1 AlatrGlyProGluSerArgLeuGluDuhertyLeuAlaMetProPheAlaThrPro 20

Qy 271 TTCAGCCCTGAAGCCGCG 254
Db 21 MetGluAlaGluLeuAla 26

RESULT 83
US-09-751-798-5
Sequence 5, Application US/09751798
Patent No. US20020010321A1
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798

FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020010321A1man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3168
TELEFAX: (212) 752-5958
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-09-751-798-5

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-751-798-5 (1-9)

Qy 522 TCCTGTGATGTGATCAGCAGTGC 548
Db 1 SerLeuMetIrrPleInrGlnCyS 9

RESULT 84
US-09-751-798-6
Sequence 6, Application US/09751798
Patent No. US20020010321A1
GENERAL INFORMATION:
APPLICANT: Stockert, Elisabeth; Jager, Elke;
APPLICANT: Chen, Yao-tseng; Scanlan, Matthew;
APPLICANT: Knuth, Alexander; Old, Lloyd J.
TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
TITLE OF INVENTION: Associated Proteins, Uses Thereof,
TITLE OF INVENTION: Truncated Forms of NY-ESO-1, and HLA
TITLE OF INVENTION: Binding Peptides Derived Therefrom
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fulbright & Jaworski, L.L.P.
STREET: 666 Fifth Avenue
CITY: New York City
STATE: New York
COUNTRY: USA
ZIP: 10103
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
COMPUTER: IBM
OPERATING SYSTEM: PC-DOS
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/751,798
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/062,422
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/725,182
FILING DATE: October 3, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Hanson, No. US20020010321A1man D.
REGISTRATION NUMBER: 30,946
REFERENCE/DOCKET NUMBER: LUD 5466.3

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-09-751-798-6

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-751-798-6 (1-9)

QY 516 CAGCTTCCCTGATGATGATCAG 542
DB 1 GlnUserSerLeuMetTrioPlethr 9

RESULT 85
US-09-766-889A-51
; Sequence 51, Application US/09766889A
; Patent No. US20020164654A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Brian
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-51

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-766-889A-51 (1-9)

QY 522 TCCTGTTGATGATGATCAGCAGTC 548
DB 1 SerLeuMetTrioPlethrGlnCys 9

RESULT 86
US-09-766-889A-52
; Sequence 52, Application US/09766889A
; Patent No. US20020164654A1
; GENERAL INFORMATION:
; APPLICANT: Luiten, Rosalie
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: van der Bruggen, Pierre

```

```

; APPLICANT: Stroobant, Vincent
; APPLICANT: Demotte, Nathalie
; APPLICANT: Schultz, Brian
; TITLE OF INVENTION: MAGE ANTIGENIC PEPTIDES WHICH BIND HLA-B35 AND HLA-B44
; FILE REFERENCE: L0461/7104
; CURRENT APPLICATION NUMBER: US/09/766,889A
; PRIOR FILING DATE: 2001-01-19
; PRIOR APPLICATION NUMBER: US 60/177,242
; PRIOR FILING DATE: 2000-01-20
; PRIOR APPLICATION NUMBER: US 60/243,212
; PRIOR FILING DATE: 2000-10-25
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 52
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-766-889A-52

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-766-889A-52 (1-9)

QY 516 CAGCTTCCCTGATGATGATCAG 542
DB 1 GlnUserSerLeuMetTrioPlethr 9

RESULT 87
US-09-833-039-19
; Sequence 19, Application US/09833039
; Publication No. US20030175960A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LND 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039-19

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039-19 (1-9)

QY 309 CGCTGCTGAGTCTACTGCGCATG 335
DB 1 ArgLeuGlnGlnPheTyrLeuAlaMet 9

```

RESULT 88
US-09-833-039-20
; Sequence 20, Application US/09833039
; Publication No. US20030175960A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039-20

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039-20 (1-9)

OY 375 AGCTGCGCCAGATGCCACCGCTT 401
Db 1 SerleuAlaGlnAspAlaProPheU 9

RESULT 89
US-09-833-039-115
; Sequence 115, Application US/09833039
; Publication No. US20030175960A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 115
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039-115

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039-115 (1-9)

OY 495 TCCATCAGCTCTGCTTCACGAGCTT 521
Db 1 SerleuSerGylsLeuGlnGlnLeu 9

RESULT 90
US-09-833-039-116
; Sequence 116, Application US/09833039
; Publication No. US20030175960A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-833-039-116

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039-116 (1-9)

OY 72 GGCACAGGCGGTTGCAGCGGATGCT 98
Db 1 GlyThrGlyGlySerThrGlyAspAla 9

RESULT 91
US-09-833-039-117
; Sequence 117, Application US/09833039
; Publication No. US20030175960A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
; FILE REFERENCE: LUD 5622.1
; CURRENT APPLICATION NUMBER: US/09/833,039
; PRIOR FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: US 09/409,455
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: US 09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 129
; SEQ ID NO 117

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/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-833-039-117

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039-117 (1-9)

QY 207 AGGCGCTGGGCGGCGAGAGCGGCC 233
Db 1 ArgAlaSerGlyProGlyGlyAla 9

RESULT 92
US-09-833-039-118
/ Sequence 118, Application US/09833039
/ Publication No. US20030175960A1
/ GENERAL INFORMATION:
/ APPLICANT: Tureci, Ozlem
/ APPLICANT: Sahin, Ugur
/ APPLICANT: Pfreundschuh, Michael
/ TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
/ FILE REFERENCE: LUD 5622.1
/ CURRENT APPLICATION NUMBER: US 09/833,039
/ CURRENT FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: US 09/409,455
/ PRIOR FILING DATE: 1999-09-30
/ PRIOR APPLICATION NUMBER: US 09/344,040
/ PRIOR FILING DATE: 1998-06-25
/ PRIOR APPLICATION NUMBER: US 09/105,839
/ PRIOR FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: US 08/851,130
/ PRIOR FILING DATE: 1997-05-05
/ NUMBER OF SEQ ID NOS: 129
/ SEQ ID NO 118
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-833-039-118

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039-118 (1-9)

QY 288 GGGGCCAGGGGCGGCGAGAGCGCCTG 314
Db 1 GlyAlaArgGlyProGluSerArgLeu 9

RESULT 93
US-09-833-039-119
/ Sequence 119, Application US/09833039
/ Publication No. US20030175960A1
/ GENERAL INFORMATION:
/ APPLICANT: Tureci, Ozlem
/ APPLICANT: Sahin, Ugur
/ APPLICANT: Pfreundschuh, Michael
/ TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
/ FILE REFERENCE: LUD 5622.1
/ CURRENT APPLICATION NUMBER: US 09/833,039
/ CURRENT FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: US 09/409,455
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/ PRIOR FILING DATE: 1999-09-30
/ PRIOR APPLICATION NUMBER: US 09/344,040
/ PRIOR FILING DATE: 1999-06-25
/ PRIOR APPLICATION NUMBER: US 09/105,839
/ PRIOR FILING DATE: 1998-06-26
/ PRIOR APPLICATION NUMBER: US 08/851,130
/ PRIOR FILING DATE: 1997-05-05
/ NUMBER OF SEQ ID NOS: 129
/ SEQ ID NO 119
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-833-039-119

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039-120 (1-9)

QY 429 TTCACGTGTCGGGACACATCACTGACT 455
Db 1 PheThrValSerGlyAsnIleLeuThr 9

RESULT 95
US-09-833-039-121
/ Sequence 121, Application US/09833039
/ Publication No. US20030175960A1
```


GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
FILE REFERENCE: LUD 5622.1
CURRENT APPLICATION NUMBER: US/09/833,039
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 09/409,455
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: US 09/344,040
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 121
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-039-121

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039-121 (1-9)

Qy 462 CTGACTGCTGACAGCAGCCGCACTG 488
Db 1 LeuNtrAlaAlaSPHisArgGlnLeu 9

RESULT 96

US-09-833-039-122
Sequence 122, Application US/09833039
Publication No. US20030175960A1
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
FILE REFERENCE: LUD 5622.1
CURRENT APPLICATION NUMBER: US/09/833,039
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 09/409,455
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: US 09/344,040
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 122
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-039-122

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039-122 (1-9)

Qy 516 CAGCTTCCCTGTGATGATGATCAG 542
Db 1 GlnNeuSerLeuMetTrpIleThr 9

RESULT 97
US-09-833-039-123
Sequence 123, Application US/09833039
Publication No. US20030175960A1
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
FILE REFERENCE: LUD 5622.1
CURRENT APPLICATION NUMBER: US/09/833,039
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 09/409,455
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: US 09/344,040
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 123
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-039-123

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039-123 (1-9)

Qy 528 TTGATGTGATCAGCAGTGTCTTG 554
Db 1 LeuMetTrpIleThrGlnCysPheLeu 9

RESULT 98
US-09-833-039-124
Sequence 124, Application US/09833039
Publication No. US20030175960A1
GENERAL INFORMATION:
APPLICANT: Tureci, Ozlem
APPLICANT: Sahin, Ugur
APPLICANT: Pfreundschuh, Michael
TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof
FILE REFERENCE: LUD 5622.1
CURRENT APPLICATION NUMBER: US/09/833,039
CURRENT FILING DATE: 2001-04-12
PRIOR APPLICATION NUMBER: US 09/409,455
PRIOR FILING DATE: 1999-09-30
PRIOR APPLICATION NUMBER: US 09/344,040
PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: US 09/105,839
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: US 08/851,130
PRIOR FILING DATE: 1997-05-05
NUMBER OF SEQ ID NOS: 129
SEQ ID NO 124
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-833-039-124

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

Alignment Scores:

Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039-124 (1-9)

QY 339 TTCGGACGCCATGAGACAGACTG 365

DB 1 PheAlaThrProMetClnAlaGluLeu 9

RESULT 99

US-09-833-039-125
; Sequence 125, Application US/09833039
; Publication No. US20030175960A1

; GENERAL INFORMATION:

; APPLICANT: Tureci, Ozlem

; APPLICANT: Sahin, Ugur

; APPLICANT: Pfrendschuh, Michael

; TITLE OF INVENTION: Tumor Associated Peptide and Uses Thereof

; FILE REFERENCE: LUD 5622.1

; CURRENT APPLICATION NUMBER: US/09/833,039

; PRIOR FILING DATE: 2001-04-12

; PRIOR APPLICATION NUMBER: US 09/409,455

; PRIOR FILING DATE: 1999-09-30

; PRIOR APPLICATION NUMBER: US 09/344,040

; PRIOR FILING DATE: 1999-06-25

; PRIOR APPLICATION NUMBER: US 09/105,839

; PRIOR FILING DATE: 1998-06-26

; PRIOR APPLICATION NUMBER: US 08/851,130

; PRIOR FILING DATE: 1997-05-05

; NUMBER OF SEQ ID NOS: 129

; SEQ ID NO 125

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-833-039-125

Alignment Scores:

Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-09-833-039-125 (1-9)

QY 432 ACTGTGCGGACACTGACTATC 458

DB 1 TmValSerGlyAsnLeuThrIle 9

RESULT 100

US-10-218-095-46
; Sequence 46, Application US/10218095
; Publication No. US20040033541A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Yi

; APPLICANT: Strobant, Vincent

; APPLICANT: Russo, Vincenzo

; APPLICANT: Boon-Falleur, Thierry

; APPLICANT: van der Bruggen, Pierre

; TITLE OF INVENTION: MAGE-A4 ANTIGENIC PEPTIDES AND USES THEREOF

; FILE REFERENCE: L00461/70137

; CURRENT APPLICATION NUMBER: US/10/218,095

; PRIOR FILING DATE: 2002-08-13

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 46

; LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

US-10-218-095-46

Alignment Scores:

Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-218-095-46 (1-9)

QY 522 TCCTGTGATGTGATGACGACG 548

DB 1 SerLeuLeuMetTrpIleThrGlnCys 9

RESULT 101

US-10-218-095-47
; Sequence 47, Application US/10218095
; Publication No. US20040033541A1

; GENERAL INFORMATION:

; APPLICANT: Zhang, Yi

; APPLICANT: Strobant, Vincent

; APPLICANT: Russo, Vincenzo

; APPLICANT: Boon-Falleur, Thierry

; APPLICANT: van der Bruggen, Pierre

; TITLE OF INVENTION: MAGE-A4 ANTIGENIC PEPTIDES AND USES THEREOF

; FILE REFERENCE: L00461/70137

; CURRENT APPLICATION NUMBER: US/10/218,095

; PRIOR FILING DATE: 2002-08-13

; NUMBER OF SEQ ID NOS: 63

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 47

; LENGTH: 9

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-218-095-47

Alignment Scores:

Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-218-095-47 (1-9)

QY 516 CAGTTTCCTGTTGATGATGACG 542

DB 1 GlnLeuSerLeuLeuMetTrpIleThr 9

RESULT 102

US-10-289-566-24
; Sequence 24, Application US/10289566
; Publication No. US20040071671A1

; GENERAL INFORMATION:

; APPLICANT: Leturcq, Didier J.

; APPLICANT: Moriarty, Ann M.

; APPLICANT: Jackson, Michael R.

; APPLICANT: Peterson, Per A.

; APPLICANT: Richards, Jon M.

; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS

; FILE REFERENCE: ORT 1342CIP

; CURRENT APPLICATION NUMBER: US/10/289,566

; PRIOR FILING DATE: 2002-11-07

; PRIOR APPLICATION NUMBER: US 60/270,252

; PRIOR FILING DATE: 2001-02-20

; PRIOR APPLICATION NUMBER: US 10/080,013

; PRIOR FILING DATE: 2002-02-19

; NUMBER OF SEQ ID NOS: 43

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; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-289-566-24

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-289-566-24 (1-9)

Qy 522 TCCTGTTGATGTGATCAGCAGTGC 548
Db 1 SerleuNeuMetTPIleThrGlnCys 9

RESULT 103
US-10-289-566-26
; Sequence 26, Application US/10289566
; Publication No. US20040071671A1
; GENERAL INFORMATION:
; APPLICANT: Leturcq, Didier J.
; APPLICANT: Moriarty, Ann M.
; APPLICANT: Jackson, Michael R.
; APPLICANT: Peterson, Per A.
; APPLICANT: Richards, Jon M.
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT 1342CIP
; CURRENT APPLICATION NUMBER: US/10/289,566
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: US 60/270,252
; PRIOR FILING DATE: 2001-02-20
; PRIOR APPLICATION NUMBER: US 10/080,013
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-289-566-26

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-289-566-26 (1-9)

Qy 516 CAGCTTTCCTGTTGATGTGATCAGC 542
Db 1 GlnleuSerleuNeuMetTPIleThr 9

RESULT 104
US-10-023-182-5
; Sequence 5, Application US/10023182
; Publication No. US2002016465A1
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; Chen, Yao-tseng; Scanlan, Matthew;
; Knuth, Alexander; Old, Lloyd J.

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; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; Associated Proteins, Uses Thereof,
; Truncated Forms of NY-ESO-1, and HLA
; Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/023,182
; FILING DATE: 17-Dec-2001
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/751,798
; FILING DATE: December 29, 2000
; APPLICATION NUMBER: 09/062,422
; FILING DATE: <unknown>
; APPLICATION NUMBER: 08/725,182
; FILING DATE: October 3, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. US2002016465A1man D.
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3168
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-023-182-5

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-023-182-5 (1-9)

Qy 522 TCCTGTTGATGTGATCAGCAGTGC 548
Db 1 SerleuNeuMetTPIleThrGlnCys 9

RESULT 105
US-10-023-182-6
; Sequence 6, Application US/10023182
; Publication No. US2002016465A1
; GENERAL INFORMATION:
; APPLICANT: Stockert, Elisabeth; Jager, Elke;
; Chen, Yao-tseng; Scanlan, Matthew;
; Knuth, Alexander; Old, Lloyd J.
; TITLE OF INVENTION: Antibodies Which Bind to NY-ESO-1 Cancer
; Associated Proteins, Uses Thereof,
; Truncated Forms of NY-ESO-1, and HLA
; Binding Peptides Derived Therefrom
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City

```

STATE: New York
 COUNTRY: USA
 ZIP: 10103
 DB:
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
 COMPUTER: IBM
 OPERATING SYSTEM: PC-DOS
 SOFTWARE: WordPerfect
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/023,182
 FILING DATE: 17-Dec-2001
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/751,798
 FILING DATE: December 29, 2000
 APPLICATION NUMBER: 09/062,422
 FILING DATE: <Unknown>
 APPLICATION NUMBER: 08/725,182
 FILING DATE: October 3, 1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Hanson, No. US2002016465A1man D.
 REGISTRATION NUMBER: 30,946
 REFERENCE/DOCKET NUMBER: LUD 5466.3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 318-3168
 TELEFAX: (212) 752-5958
 INFORMATION FOR SEQ ID NO: 6:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 US-10-023-182-6
 SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Alignment Scores:

Pred. No.: 267 Length: 9
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.00% Indels: 0
 DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-023-182-6 (1-9)

Qy 516 CAGCTTCCCTGTGATGTGATCAGC 542
 Db 1 GinLeuSerLeuMetTrpIleThr 9

RESULT 106

US-10-274-017-1
 ; Sequence 1, Application US/10274017
 ; Publication No. US20030050451A1
 ; GENERAL INFORMATION:
 ; LUD-5668-PCT
 ; APPLICANT: Gnjatlic, Sacha
 ; APPLICANT: Old, Lloyd J.
 ; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA-C MOLECULES AND USES
 ; FILE REFERENCE: THEREOF
 ; CURRENT APPLICATION NUMBER: US/10/274,017
 ; CURRENT FILING DATE: 2002-10-18
 ; PRIOR APPLICATION NUMBER: US/09/670,456
 ; PRIOR FILING DATE: 2001-09-26
 ; NUMBER OF SEQ ID NOS: 5
 ; SEQ ID NO 1
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-274-017-1

Alignment Scores:

Pred. No.: 267 Length: 9
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.00% Indels: 0
 DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-274-017-1 (1-9)

Qy 522 TCCTGTGATGTGATCAGCAGTGC 548
 Db 1 SerLeuMetTrpIleThrGlnCys 9

RESULT 107

US-10-274-017-2
 ; Sequence 2, Application US/10274017
 ; Publication No. US20030050451A1
 ; GENERAL INFORMATION:
 ; LUD-5668-PCT
 ; APPLICANT: Gnjatlic, Sacha
 ; APPLICANT: Old, Lloyd J.
 ; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA-C MOLECULES AND USES
 ; FILE REFERENCE: THEREOF
 ; CURRENT APPLICATION NUMBER: US/10/274,017
 ; CURRENT FILING DATE: 2002-10-18
 ; PRIOR APPLICATION NUMBER: US/09/670,456
 ; PRIOR FILING DATE: 2001-09-26
 ; NUMBER OF SEQ ID NOS: 5
 ; SEQ ID NO 2
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-274-017-2

Alignment Scores:

Pred. No.: 267 Length: 9
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.00% Indels: 0
 DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-274-017-2 (1-9)

Qy 327 CTCGGCATGCCTTTGCGACACCCATG 353
 Db 1 LeuAlaMetProPheAlaThrPromet 9

RESULT 108

US-10-274-017-3
 ; Sequence 3, Application US/10274017
 ; Publication No. US20030050451A1
 ; GENERAL INFORMATION:
 ; LUD-5668-PCT
 ; APPLICANT: Gnjatlic, Sacha
 ; APPLICANT: Old, Lloyd J.
 ; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA-C MOLECULES AND USES
 ; FILE REFERENCE: THEREOF
 ; CURRENT APPLICATION NUMBER: US/10/274,017
 ; CURRENT FILING DATE: 2002-10-18
 ; PRIOR APPLICATION NUMBER: US/09/670,456
 ; PRIOR FILING DATE: 2001-09-26
 ; NUMBER OF SEQ ID NOS: 5
 ; SEQ ID NO 3
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-274-017-3

Alignment Scores:

Pred. No.: 267 Length: 9
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0

Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-274-017-3 (1-9)
QY 291 GCCAGGGGGCGGAGAGCGGCTGCTT 317
DB 1 A1a1g1g1yProgluSerArgLeuLeu 9
RESULT 109
US-10-080-013-24
; Sequence 24, Application US/10080013
; Publication No. US20030077248A1
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Lecurcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: US/10/080,013
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-013-24
Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-080-013-24 (1-9)
QY 522 TCCTGTGATGTGATCAGCAGTGC 548
DB 1 SerleuemetTptletThrGlnCys 9
RESULT 110
US-10-080-013-26
; Sequence 26, Application US/10080013
; Publication No. US20030077248A1
; GENERAL INFORMATION:
; APPLICANT: Moriarty, Ann
; APPLICANT: Lecurcq, Didier
; APPLICANT: Degraw, Juli
; APPLICANT: Heiskala, Marja
; APPLICANT: Peterson, Per
; APPLICANT: Jackson, Michael
; TITLE OF INVENTION: A CELL THERAPY METHOD FOR THE TREATMENT OF TUMORS
; FILE REFERENCE: ORT-1557
; CURRENT APPLICATION NUMBER: US/10/080,013
; CURRENT FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-080-013-26
Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-080-013-26 (1-9)
QY 516 CAGCTTTCCTGTGATGTGATCAGC 542
DB 1 GlnleuSerleuemetTptletThr 9
RESULT 111
US-10-161-097-34
; Sequence 34, Application US/10161097
; Publication No. US20030096404A1
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/10/161,097
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US/09/574,749
; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 34
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-10-161-097-34
Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-161-097-34 (1-9)
QY 522 TCCTGTGATGTGATCAGCAGTGC 548
DB 1 SerleuemetTptletThrGlnCys 9
RESULT 112
US-10-161-097-35
; Sequence 35, Application US/10161097
; Publication No. US20030096404A1
; GENERAL INFORMATION:
; APPLICANT: ROSENZWEIG, Michael
; APPLICANT: PYKETT, Mark J.
; APPLICANT: SCADEN, David T.
; APPLICANT: POZNANSKY, Mark C.
; TITLE OF INVENTION: LYMPHOID TISSUE-SPECIFIC CELL PRODUCTION
; TITLE OF INVENTION: FROM HEMATOPOIETIC PROGENITOR CELLS IN THREE-DIMENSIONAL
; FILE REFERENCE: C1005/7012/KA/ERG
; CURRENT APPLICATION NUMBER: US/10/161,097
; CURRENT FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US/09/574,749

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; PRIOR FILING DATE: 2002-05-31
; PRIOR APPLICATION NUMBER: US 60/107,972
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: PCT/US99/26795
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/524,749
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Homo Sapiens source
US-10-161-097-35

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00            Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-161-097-35 (1-9)

QY 516 CAGCTTCCTGCTGATGATGCACG 542
DB 1 GlnleuSerleuMettriplethr 9

RESULT 113
US-10-170-832-80
; Sequence 80, Application US/10170832
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vancomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Cortbals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/10/170,832
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 80
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-832-80

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00            Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-170-832-80 (1-9)

QY 522 TCCTGTGATGTGATGCACGAGTGC 548
DB 1 SerleuMettriplethrGlnCys 9

RESULT 114
US-10-170-832-81
```

```

; Sequence 81, Application US/10170832
; Publication No. US20030170792A1
; GENERAL INFORMATION:
; APPLICANT: Chaux, Pascal
; APPLICANT: Vancomme, Valrie
; APPLICANT: Stroobant, Vincent
; APPLICANT: Boon-Falleur, Thierry
; APPLICANT: van der Bruggen, Pierre
; APPLICANT: Thielemans, Kris
; APPLICANT: Cortbals, Jurgen
; TITLE OF INVENTION: MAGE-3 PEPTIDES PRESENTED BY HLA CLASS II MOLECULES
; FILE REFERENCE: L0461/7052
; CURRENT APPLICATION NUMBER: US/10/170,832
; CURRENT FILING DATE: 2002-06-12
; PRIOR APPLICATION NUMBER: US/09/166,448
; PRIOR FILING DATE: 1998-10-05
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 81
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-170-832-81

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00            Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-170-832-81 (1-9)

QY 516 CAGCTTCCTGCTGATGATGCACG 542
DB 1 GlnleuSerleuMettriplethr 9

RESULT 115
US-10-364-614-1
; Sequence 1, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: Gnjatic, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 CIP
; CURRENT APPLICATION NUMBER: US/10/364,614
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-1

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00            Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-364-614-1 (1-9)

QY 333 ATGCCCTTCGGACACCCCATGGAACA 359
DB 1 ATGCCCTTCGGACACCCCATGGAACA 359
```

Db 1 MetProhealathrPrometGluA1a 9

RESULT 116

US-10-364-614-2

Sequence 2, Application US/10364614

Publication No. US20030175250A1

GENERAL INFORMATION:

APPLICANT: JAGER, Elke

APPLICANT: KNUTH, Alexander

APPLICANT: OLD, Lloyd

APPLICANT: Gnajatic, Sacha

TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF

FILE REFERENCE: LUD 5726.1 CIP

CURRENT APPLICATION NUMBER: US/10/364,614

CURRENT FILING DATE: 2003-02-24

PRIOR APPLICATION NUMBER: US 60/355,828

PRIOR FILING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

US-10-364-614-2

Alignment Scores:

Pred. No.: 267 Length: 9

Score: 9.00 Matches: 9

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 5.00% Indels: 0

DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-364-614-2 (1-9)

QY 330 GCCATGCTTTCGCGACACCCATGGAA 356

Db 1 AlameTProhealathrPrometGlu 9

RESULT 117

US-10-364-614-3

Sequence 3, Application US/10364614

Publication No. US20030175250A1

GENERAL INFORMATION:

APPLICANT: JAGER, Elke

APPLICANT: KNUTH, Alexander

APPLICANT: OLD, Lloyd

APPLICANT: Gnajatic, Sacha

TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF

FILE REFERENCE: LUD 5726.1 CIP

CURRENT APPLICATION NUMBER: US/10/364,614

CURRENT FILING DATE: 2003-02-24

PRIOR APPLICATION NUMBER: US 60/355,828

PRIOR FILING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.2

SEQ ID NO 3

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

US-10-364-614-3

Alignment Scores:

Pred. No.: 267 Length: 9

Score: 9.00 Matches: 9

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 5.00% Indels: 0

DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-364-614-3 (1-9)

QY 375 AGCTGCGCCAGATGCCACCGCTT 401

Db 1 SerleuAlaGlnsPalapProleu 9

RESULT 118

US-10-364-614-4

Sequence 4, Application US/10364614

Publication No. US20030175250A1

GENERAL INFORMATION:

APPLICANT: JAGER, Elke

APPLICANT: KNUTH, Alexander

APPLICANT: OLD, Lloyd

APPLICANT: Gnajatic, Sacha

TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF

FILE REFERENCE: LUD 5726.1 CIP

CURRENT APPLICATION NUMBER: US/10/364,614

CURRENT FILING DATE: 2003-02-24

PRIOR APPLICATION NUMBER: US 60/355,828

PRIOR FILING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.2

SEQ ID NO 4

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

US-10-364-614-4

Alignment Scores:

Pred. No.: 267 Length: 9

Score: 9.00 Matches: 9

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 5.00% Indels: 0

DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-364-614-4 (1-9)

QY 324 TACCTGCGCATGCTTTCGCGACACCC 350

Db 1 TyrlenuAlameTProhealathrPro 9

RESULT 119

US-10-364-614-8

Sequence 8, Application US/10364614

Publication No. US20030175250A1

GENERAL INFORMATION:

APPLICANT: JAGER, Elke

APPLICANT: KNUTH, Alexander

APPLICANT: OLD, Lloyd

APPLICANT: Gnajatic, Sacha

TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF

FILE REFERENCE: LUD 5726.1 CIP

CURRENT APPLICATION NUMBER: US/10/364,614

CURRENT FILING DATE: 2003-02-24

PRIOR APPLICATION NUMBER: US 60/355,828

PRIOR FILING DATE: 2002-02-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: PatentIn version 3.2

SEQ ID NO 8

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

US-10-364-614-8

Alignment Scores:

Pred. No.: 267 Length: 9

Score: 9.00 Matches: 9

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 5.00% Indels: 0

DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-364-614-8 (1-9)

QY 327 CTCGCCATGCTTTGGCGACACCCATG 353
Db 1 LeuAlaMetProPheAlaThrProMet 9
RESULT 120
US-10-364-614-10
; Sequence 10, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: Gnathic, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 CIP
; CURRENT APPLICATION NUMBER: US/10/364,614
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-10
Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-364-614-10 (1-9)
QY 522 TCCCTGTTGATGTGATCGCAGTGC 548
Db 1 SerLeuMetLeuMetTrpIleThrGlnCys 9
RESULT 121
US-10-364-614-11
; Sequence 11, Application US/10364614
; Publication No. US20030175250A1
; GENERAL INFORMATION:
; APPLICANT: JAGER, Elke
; APPLICANT: KNUTH, Alexander
; APPLICANT: OLD, Lloyd
; APPLICANT: Gnathic, Sacha
; TITLE OF INVENTION: ISOLATED PEPTIDES WHICH BIND TO HLA MOLECULES AND USES THEREOF
; FILE REFERENCE: LUD 5726.1 CIP
; CURRENT APPLICATION NUMBER: US/10/364,614
; CURRENT FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: US 60/355,828
; PRIOR FILING DATE: 2002-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-364-614-11
Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-364-614-11 (1-9)

QY 516 CAGCTTTCCTGTTGATGTGATCAG 542
Db 1 GlnLeuSerLeuMetTrpIleThr 9
RESULT 122
US-10-239-313A-466
; Sequence 466, Application US/10239313A
; Publication No. US20030175285A1
; GENERAL INFORMATION:
; APPLICANT: KLINGUER - HAMOUR, Christine
; APPLICANT: CORVAIA, Nathalie
; APPLICANT: BECK, Alain
; APPLICANT: GOETSCH, Liliane
; TITLE OF INVENTION: MOLECULE OF PHARMACEUTICAL INTEREST COMPRISING AT ITS
; TITLE OF INVENTION: N-TERMINAL A GLUTAMIC ACID OR A GLUTAMINE IN THE FORM
; FILE REFERENCE: 343 727 - US
; CURRENT APPLICATION NUMBER: US/10/239,313A
; CURRENT FILING DATE: 2002-09-19
; PRIOR APPLICATION NUMBER: FR 00/03711
; PRIOR FILING DATE: 2000-03-23
; PRIOR APPLICATION NUMBER: PCT 01/70772
; PRIOR FILING DATE: 2001-03-22
; NUMBER OF SEQ ID NOS: 697
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 466
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-239-313A-466
Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-239-313A-466 (1-9)
QY 516 CAGCTTTCCTGTTGATGTGATCAG 542
Db 1 GlnLeuSerLeuMetTrpIleThr 9
RESULT 123
US-10-177-277-19
; Sequence 19, Application US/10177277
; Publication No. US20030185844A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfeundschnuh, Michael
; APPLICANT: Ramenese, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determini
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 19
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens


```
US-10-177-277-19
Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-177-277-19 (1-9)
OY 309 CGCCTGCTGAGTCTTACCTCGCAGT 335
DB 1 ArgLeuLeuGluPheTyrLeuAlaMet 9

RESULT 124
US-10-177-277-20
; Sequence 20, Application US/10177277
; Publication No. US20030185844A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stefanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 20
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-20

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-177-277-20 (1-9)
OY 375 AGCCTGCGCCAGATGCCCGCCTT 401
DB 1 SerLeuAlaGlnAspAlaProPheLeu 9

RESULT 125
US-10-177-277-115
; Sequence 115, Application US/10177277
; Publication No. US20030185844A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stefanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
```

```
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 115
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-115

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-177-277-115 (1-9)
OY 72 GGCACAGGGGCTTGACGGCGAGCT 98
DB 1 GlyThrGlySerThrGlyAspAla 9

RESULT 127

US-10-177-277-116
; Sequence 116, Application US/10177277
; Publication No. US20030185844A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stefanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene at
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 116
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-116

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
```

US-10-177-277-117
 ; Sequence 117, Application US/10177277
 ; Publication No. US20030185844A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tureci, Ozlem
 ; APPLICANT: Sahin, Ugur
 ; APPLICANT: Pfreundschuh, Michael
 ; APPLICANT: Ramensee, Hans Georg
 ; APPLICANT: Stevanovic, Stefan
 ; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
 ; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
 ; FILE REFERENCE: LUD 5556.1
 ; CURRENT APPLICATION NUMBER: US/10/177, 277
 ; CURRENT FILING DATE: 2002-06-21
 ; PRIOR APPLICATION NUMBER: US/09/344, 040
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: US 09/105, 839
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 08/851, 130
 ; PRIOR FILING DATE: 1997-05-05
 ; NUMBER OF SEQ ID NOS: 132
 ; SEQ ID NO 117
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-177-277-117

Alignment Scores:
 Pred. No.: 267 Length: 9
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.00% Indels: 0
 DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-177-277-117 (1-9)

Qy 207 AGGGCCTCGGGCCGGAGAGCGCC 233
 Db 1 ArgAlaSerGlyProGlyGlyAla 9

RESULT 128
 US-10-177-277-118
 ; Sequence 118, Application US/10177277
 ; Publication No. US20030185844A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tureci, Ozlem
 ; APPLICANT: Sahin, Ugur
 ; APPLICANT: Pfreundschuh, Michael
 ; APPLICANT: Ramensee, Hans Georg
 ; APPLICANT: Stevanovic, Stefan
 ; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
 ; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
 ; FILE REFERENCE: LUD 5556.1
 ; CURRENT APPLICATION NUMBER: US/10/177, 277
 ; CURRENT FILING DATE: 2002-06-21
 ; PRIOR APPLICATION NUMBER: US/09/344, 040
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: US 09/105, 839
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 08/851, 130
 ; PRIOR FILING DATE: 1997-05-05
 ; NUMBER OF SEQ ID NOS: 132
 ; SEQ ID NO 118
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-177-277-118

Alignment Scores:
 Pred. No.: 267 Length: 9

Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.00% Indels: 0
 DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-177-277-118 (1-9)

Qy 288 GGGGCCAGGGCCGGAGAGCGCCCTG 314
 Db 1 GlyAlaArgGlyProGlySerArgLeu 9

RESULT 129
 US-10-177-277-119
 ; Sequence 119, Application US/10177277
 ; Publication No. US20030185844A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tureci, Ozlem
 ; APPLICANT: Sahin, Ugur
 ; APPLICANT: Pfreundschuh, Michael
 ; APPLICANT: Ramensee, Hans Georg
 ; APPLICANT: Stevanovic, Stefan
 ; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
 ; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
 ; FILE REFERENCE: LUD 5556.1
 ; CURRENT APPLICATION NUMBER: US/10/177, 277
 ; CURRENT FILING DATE: 2002-06-21
 ; PRIOR APPLICATION NUMBER: US/09/344, 040
 ; PRIOR FILING DATE: 1999-06-25
 ; PRIOR APPLICATION NUMBER: US 09/105, 839
 ; PRIOR FILING DATE: 1998-06-26
 ; PRIOR APPLICATION NUMBER: US 08/851, 130
 ; PRIOR FILING DATE: 1997-05-05
 ; NUMBER OF SEQ ID NOS: 132
 ; SEQ ID NO 119
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-177-277-119

Alignment Scores:
 Pred. No.: 267 Length: 9
 Score: 9.00 Matches: 9
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.00% Indels: 0
 DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-177-277-119 (1-9)

Qy 342 GCGACACCATGAGAGAGCTGGCC 368
 Db 1 AlaThrProMetGluAlaGluLeuAla 9

RESULT 130
 US-10-177-277-120
 ; Sequence 120, Application US/10177277
 ; Publication No. US20030185844A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Tureci, Ozlem
 ; APPLICANT: Sahin, Ugur
 ; APPLICANT: Pfreundschuh, Michael
 ; APPLICANT: Ramensee, Hans Georg
 ; APPLICANT: Stevanovic, Stefan
 ; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determin
 ; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
 ; FILE REFERENCE: LUD 5556.1
 ; CURRENT APPLICATION NUMBER: US/10/177, 277
 ; CURRENT FILING DATE: 2002-06-21
 ; PRIOR APPLICATION NUMBER: US/09/344, 040
 ; PRIOR FILING DATE: 1999-06-25

```
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 120
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-120

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-177-277-120 (1-9)

QY 429 TTCACGTGTCGGCAGACTGACT 455
Db 1 PheThrValSerGlyAsnIleLeuThr 9

RESULT 131
US-10-177-277-121
; Sequence 121, Application US/10177277
; Publication No. US20030185844A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Ramenese, Hans Georg
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Stefanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 121
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-121

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-177-277-121 (1-9)

QY 462 CTGACTGCTGCAGACCGCCCACTG 488
Db 1 LeuThrAlaAlaAspHisArgGlnLeu 9

RESULT 132
US-10-177-277-122
; Sequence 122, Application US/10177277
; Publication No. US20030185844A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Ramenese, Hans Georg
; APPLICANT: Stefanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 122
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-122

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-177-277-122 (1-9)

QY 516 CAGCTTCCCTGTGATGATGATCAGC 542
Db 1 GlnUeSerLeuUeuMetTrpIleThr 9

RESULT 133
US-10-177-277-123
; Sequence 123, Application US/10177277
; Publication No. US20030185844A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Ramenese, Hans Georg
; APPLICANT: Pfreundschuh, Michael
; APPLICANT: Stefanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer In a Sample By Determini
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene ar
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 123
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-123

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%      Indels: 0
```

DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-177-277-123 (1-9)
QY 528 TTGATGTGATCAGCAGCTTCTG 554
DB 1 LeuMetIrrPleThrGlnCysPheLeu 9
RESULT 134
US-10-177-277-124
; Sequence 124, Application US/10177277
; Publication No. US20030185844A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendenschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determining
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 124
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-124
Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-177-277-124 (1-9)
QY 339 TTCGGCAGCCCATGAGCAGCTG 365
DB 1 PheAlaIrrPleThrGlnGluIleLeu 9
RESULT 135
US-10-177-277-125
; Sequence 125, Application US/10177277
; Publication No. US20030185844A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendenschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determining
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05

; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 125
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-125
Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-177-277-125 (1-9)
QY 432 ACTGTGTCGGCACTACTGACTATC 458
DB 1 ThrValSerGlyAsnIleLeuThrIle 9
RESULT 136
US-10-177-277-131
; Sequence 131, Application US/10177277
; Publication No. US20030185844A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendenschuh, Michael
; APPLICANT: Ramensee, Hans Georg
; APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determining
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/177,277
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 131
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-131
Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-177-277-131 (1-9)
QY 522 TCCTGTGTGATGTGATCAGCAGCTGC 548
DB 1 SerLeuMetIrrPleThrGlnCys 9
RESULT 137
US-10-177-277-132
; Sequence 132, Application US/10177277
; Publication No. US20030185844A1
; GENERAL INFORMATION:
; APPLICANT: Tureci, Ozlem
; APPLICANT: Sahin, Ugur
; APPLICANT: Pfrendenschuh, Michael
; APPLICANT: Ramensee, Hans Georg

```
APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/117,277
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-132

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-177-277-132 (1-9)

Qy 516 CAGCTTCCCTGTTGATGATCAG 542
Db 1 GlnLeuSerLeuLeuMetTyrIleThr 9

RESULT 138
US-10-117-937-169
; Sequence 169, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 169
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-169

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-169 (1-9)

Qy 297 GGGCGGAGAGCGCGCTGCTGAGTTC 323
Db 1 GlnLeuSerLeuLeuMetTyrIleThr 9
```

```
APPLICANT: Stevanovic, Stefan
; TITLE OF INVENTION: Method for Determining Presence of Cancer in a Sample By Determin
; TITLE OF INVENTION: Expression of an SSX Gene, Peptides Derived From Said SSX Gene a
; TITLE OF INVENTION: Gene, and Uses Thereof
; FILE REFERENCE: LUD 5556.1
; CURRENT APPLICATION NUMBER: US/10/117,277
; PRIOR FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US/09/344,040
; PRIOR FILING DATE: 1999-06-25
; PRIOR APPLICATION NUMBER: US 09/105,839
; PRIOR FILING DATE: 1998-06-26
; PRIOR APPLICATION NUMBER: US 08/851,130
; PRIOR FILING DATE: 1997-05-05
; NUMBER OF SEQ ID NOS: 132
; SEQ ID NO 132
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-277-132

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00%  Conservative: 0
Best Local Similarity: 100.00%  Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-170 (1-9)

Qy 300 CCGAGAGCGCGCTGCTGAGTTCAC 326
Db 1 ProGlnSerArgLeuLeuGluPheTyr 9

RESULT 140
US-10-117-937-172
; Sequence 172, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 172
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-172
```

Alignment Scores:		267	Length:	9
Pred. No.:	9.00	Matches:	9	
Score:	100.00%	Conservative:	0	
Percent Similarity:	100.00%	Mismatches:	0	
Best Local Similarity:	100.00%	Indels:	0	
Query Match:	5.00%	Gaps:	0	
DB:	1			
US-10-023-182-1 (1-752) x US-10-117-937-172 (1-9)				
QY 303 GAGAGCCGCTTGAGTTCTACTC 329				
DB 1 ArgLeuLeuGluPheTyrLeuAlaMet 9				
RESULT 141				
US-10-117-937-173				
Sequence 173, Application US/10117937				
Publication No. US20030220239A1				
GENERAL INFORMATION:				
APPLICANT: CTL IMMUNO THERAPIES CORP.				
APPLICANT: SIMARD, John, J.L.				
APPLICANT: DIAMOND, David, C.				
APPLICANT: LIU, Liping				
APPLICANT: XIE, Zhidong				
TITLE OF INVENTION: EPTIPE SEQUENCES				
FILE REFERENCE: CTILIM.027A				
CURRENT APPLICATION NUMBER: US/10/117,937				
CURRENT FILING DATE: 2002-04-04				
PRIOR APPLICATION NUMBER: US 60/282,211				
PRIOR FILING DATE: 2001-04-06				
PRIOR APPLICATION NUMBER: US 60/337,017				
PRIOR FILING DATE: 2001-11-07				
PRIOR APPLICATION NUMBER: US 60/363,210				
PRIOR FILING DATE: 2002-03-07				
NUMBER OF SEQ ID NOS: 602				
SOFTWARE: FastSeq for Windows Version 4.0				
SEQ ID NO 173				
LENGTH: 9				
TYPE: PRT				
ORGANISM: Homo sapiens				
US-10-117-937-173				
Alignment Scores:				
Pred. No.:	267	Length:	9	
Score:	9.00	Matches:	9	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	5.00%	Indels:	0	
DB:	1	Gaps:	0	
US-10-023-182-1 (1-752) x US-10-117-937-173 (1-9)				
QY 309 CGCCTGCTTGAGTTCTACTCGGCATG 335				
DB 1 ArgLeuLeuGluPheTyrLeuAlaMet 9				
RESULT 142				
US-10-117-937-174				
Sequence 174, Application US/10117937				
Publication No. US20030220239A1				
GENERAL INFORMATION:				
APPLICANT: CTL IMMUNO THERAPIES CORP.				
APPLICANT: SIMARD, John, J.L.				
APPLICANT: DIAMOND, David, C.				
APPLICANT: LIU, Liping				
APPLICANT: XIE, Zhidong				
TITLE OF INVENTION: EPTIPE SEQUENCES				
FILE REFERENCE: CTILIM.027A				
CURRENT APPLICATION NUMBER: US/10/117,937				
CURRENT FILING DATE: 2002-04-04				
PRIOR APPLICATION NUMBER: US 60/282,211				
PRIOR FILING DATE: 2001-04-06				
PRIOR APPLICATION NUMBER: US 60/337,017				
PRIOR FILING DATE: 2001-11-07				
NUMBER OF SEQ ID NOS: 602				
SOFTWARE: FastSeq for Windows Version 4.0				
SEQ ID NO 177				
LENGTH: 9				
TYPE: PRT				
ORGANISM: Homo sapiens				
US-10-117-937-177				
Alignment Scores:				
Pred. No.:	267	Length:	9	
Score:	9.00	Matches:	9	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	5.00%	Indels:	0	
DB:	1	Gaps:	0	
US-10-023-182-1 (1-752) x US-10-117-937-177 (1-9)				
QY 333 ATGCTTTCGAGACCATGGAAGCA 359				
DB 1 MetProPheAlaThrProMetGluAla 9				
RESULT 144				
US-10-117-937-178				
Sequence 178, Application US/10117937				
Publication No. US20030220239A1				
GENERAL INFORMATION:				
APPLICANT: CTL IMMUNO THERAPIES CORP.				
PRIOR FILING DATE: 2001-11-07				
PRIOR APPLICATION NUMBER: US 60/363,210				
PRIOR FILING DATE: 2002-03-07				
NUMBER OF SEQ ID NOS: 602				
SOFTWARE: FastSeq for Windows Version 4.0				
SEQ ID NO 177				
LENGTH: 9				
TYPE: PRT				
ORGANISM: Homo sapiens				
US-10-117-937-177				
Alignment Scores:				
Pred. No.:	267	Length:	9	
Score:	9.00	Matches:	9	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	5.00%	Indels:	0	
DB:	1	Gaps:	0	
US-10-023-182-1 (1-752) x US-10-117-937-177 (1-9)				
QY 315 CTGAGTTCTACCTCGGCATGCTTTC 341				
DB 1 LeuGluPheTyrLeuAlaMetProPhe 9				
RESULT 143				
US-10-117-937-177				
Sequence 177, Application US/10117937				
Publication No. US20030220239A1				
GENERAL INFORMATION:				
APPLICANT: CTL IMMUNO THERAPIES CORP.				
APPLICANT: SIMARD, John, J.L.				
APPLICANT: DIAMOND, David, C.				
APPLICANT: LIU, Liping				
APPLICANT: XIE, Zhidong				
TITLE OF INVENTION: EPTIPE SEQUENCES				
FILE REFERENCE: CTILIM.027A				
CURRENT APPLICATION NUMBER: US/10/117,937				
CURRENT FILING DATE: 2002-04-04				
PRIOR APPLICATION NUMBER: US 60/282,211				
PRIOR FILING DATE: 2001-04-06				
PRIOR APPLICATION NUMBER: US 60/337,017				
PRIOR FILING DATE: 2001-11-07				
PRIOR APPLICATION NUMBER: US 60/363,210				
PRIOR FILING DATE: 2002-03-07				
NUMBER OF SEQ ID NOS: 602				
SOFTWARE: FastSeq for Windows Version 4.0				
SEQ ID NO 177				
LENGTH: 9				
TYPE: PRT				
ORGANISM: Homo sapiens				
US-10-117-937-177				
Alignment Scores:				
Pred. No.:	267	Length:	9	
Score:	9.00	Matches:	9	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	5.00%	Indels:	0	
DB:	1	Gaps:	0	
US-10-023-182-1 (1-752) x US-10-117-937-174 (1-9)				
QY 315 CTGAGTTCTACCTCGGCATGCTTTC 341				
DB 1 LeuGluPheTyrLeuAlaMetProPhe 9				
RESULT				

```

; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPTOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 178
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-178

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00            Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-178 (1-9)
QY 396 CCGCTTCCGCGCAGGGGTGCTCTG 422
Db 1 1 ProlenProvalProGlyValLeuLeu 9

RESULT 145
US-10-117-937-182
; Sequence 182, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPTOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-182

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00            Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-182 (1-9)
QY 396 CCGCTTCCGCGCAGGGGTGCTCTG 422
Db 1 1 ProlenProvalProGlyValLeuLeu 9
```

```

QY 405 GTGCCAGGGGTGCTTGAAGAGTTC 431
Db 1 1 ValProGlyValLeuLeuGlyGluPhe 9

RESULT 146
US-10-117-937-185
; Sequence 185, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPTOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-185

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00            Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-185 (1-9)
QY 432 ACTGTGTCGCGACATACGACTATC 458
Db 1 1 ThrValSerGlyAsnIleLeuThrIle 9

RESULT 147
US-10-117-937-187
; Sequence 187, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPTOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 187
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
```

```

; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 190
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-190

Alignment Scores:
Pred. No.: 267
Score: 9.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.00%
DB: 1
Gaps:

US-10-023-182-1 (1-752) x US-10-117-937-190 (1-9)
OY 405 GTCGACGAGGCTCTCTGACGAGTTC 431
|||
Db 1 ValProGlyValLeuLeuLeuGluPhe 9

RESULT 150
US-10-117-937-192
; Sequence 192, Application US/10117937
; Publication No. US20030220239A1
GENERAL INFORMATION:
; APPLICANT: CITI IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liding
; APPLICANT: XIE, Zhidong
TITLE OR INVENTION: EPTOPE SEQUENCES
FILE REFERENCE: CTL1MM-027A
CURRENT APPLICATION NUMBER: US/10/117,937
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/282,211
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/337,017
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: US 60/363,210
PRIOR FILING DATE: 2002-03-07
NUMBER OF SEQ ID NOS: 602
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 192
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-10-117-937-192

Alignment Scores:
Pred. No.: 267
Score: 9.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 5.00%
DB: 1
Gaps:

US-10-023-182-1 (1-752) x US-10-117-937-192 (1-9)
OY 468 GTCGACGACGACCGGACGACTGCAGGTC 494
|||
Db 1 AlaAlaAspHisArgGlnLeuGlnLeu 9

RESULT 151
US-10-117-937-193
; Sequence 193, Application US/10117937
; Publication No. US20030220239A1

```



```

; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 193
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-193

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-193 (1-9)
QY 495 TCATCAGCTCTCTGTCTCAGCAGCTT 521
Db 1 SerleSeSerCyLeuGInGInLeu 9

RESULT 152
US-10-117-937-196
; Sequence 196, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 196
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-196

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
```

```

US-10-023-182-1 (1-752) x US-10-117-937-196 (1-9)
QY 534 TCATCAGCAGGCTTCTGCGCCGTG 560
Db 1 TptleThrgInCysPheLeuProVal 9

RESULT 153
US-10-117-937-197
; Sequence 197, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 197
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-197

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-197 (1-9)
QY 522 TCCTGTGATGTGATCAGCAGTC 548
Db 1 SerleuSeuMetTptleThrgInCys 9

RESULT 154
US-10-117-937-198
; Sequence 198, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 198
; LENGTH: 9
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-198

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-198 (1-9)

QY 501 AGCTCTCTCTCCAGAGCTTTCCTG 527
DB 1 SerSerCysLeuGlnGlnLeuSerLeu 9

RESULT 155
US-10-117-937-199
; Sequence 199, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-199

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-199 (1-9)

QY 513 CAGCAGCTTTCCTGTTGATGTGATC 539
DB 1 GlnGlnLeuSerLeuLeuMetTrpIle 9

RESULT 156
US-10-117-937-200
; Sequence 200, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
```

```
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-200

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-200 (1-9)

QY 504 TCTGTCTTCAGAGCTTTCCTGTG 530
DB 1 SerCysLeuGlnGlnLeuSerLeuLeu 9

RESULT 157
US-10-117-937-202
; Sequence 202, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-202

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00           Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-202 (1-9)

QY 540 ACGAGTGCTTTCGCCGTTGTTTG 566
DB 1 ThrGlnCysPheLeuProValPheLeu 9

RESULT 158
US-10-117-937-354
```

```
; Sequence 354, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 354
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-354

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00            Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-354 (1-9)
OY 252 GCGCGGCTTCAGGCTGATGATGC 278
Db 1 G|Y|A|A|A|S|e|r|G|y|L|e|u|h|e|n|g|y|C|y|s 9

RESULT 159
US-10-117-937-355
; Sequence 355, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 355
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-355

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00            Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00%     Indels: 0
DB: 1                  Gaps: 0
```

```
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-355 (1-9)
OY 207 AGGCGCTCGGGCGCGGAGAGAGCGCC 233
Db 1 A|r|g|A|A|S|e|r|G|y|P|r|o|G|y|G|y|A|A 9

RESULT 160
US-10-117-937-356
; Sequence 356, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPITOPE SEQUENCES
; FILE REFERENCE: CTLIMM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 356
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-356

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00            Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00%      Indels: 0
DB: 1                  Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-356 (1-9)
OY 243 CCGCATGGCGGCGCGGCTTCAGGCGCTG 269
Db 1 P|r|h|i|s|t|S|e|r|G|y|A|A|A|S|e|r|G|y|L|e|u 9

RESULT 161
US-10-164-121A-15
; Sequence 15, Application US/10164121A
; Publication No. US20030228308A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Boon, Thierry
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Traversari, Catra
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereof
; FILE REFERENCE: IUD-5771
; CURRENT APPLICATION NUMBER: US/10/164,121A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 15
; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
US-10-164-121A-15

Alignment Scores:
Pred. No.: 267          Length: 9
Score: 9.00            Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00%     Indels: 0
DB: 1                  Gaps: 0
```

Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-164-121A-15 (1-9)

QY 522 TCCTGTGTGATGATCAGCAGTGC 548
DB 1 SerleuMetPrlrThrGlnCys 9

RESULT 162
US-10-164-121A-24
; Sequence 24, Application US/10164121A
; Publication No. US20030228308A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Boon, Thierry
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Traversari, Catia
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5771
; CURRENT APPLICATION NUMBER: US/10/164,121A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-121A-24

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-164-121A-24 (1-9)

QY 327 CTCGCCATGCTTTTCGACACCCATG 353
DB 1 LeuAlaMetProPheAlaThrProMet 9

RESULT 163
US-10-164-121A-25
; Sequence 25, Application US/10164121A
; Publication No. US20030228308A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Yi
; APPLICANT: Boon, Thierry
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Traversari, Catia
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-Cw6 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5771
; CURRENT APPLICATION NUMBER: US/10/164,121A
; CURRENT FILING DATE: 2002-08-26
; NUMBER OF SEQ ID NOS: 36
; SEQ ID NO 25
; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-121A-25

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-164-121A-25 (1-9)

QY 291 GCCAGGGGGCCGAGAGCCGCTGCTT 317
DB 1 AlaArgGlyProGlnUserArgLeuLeu 9

RESULT 164
US-10-164-078A-14
; Sequence 14, Application US/10164078A
; Publication No. US20030228325A1
; GENERAL INFORMATION:
; APPLICANT: Bilsborough, Janine
; APPLICANT: Schultz, Erwin
; APPLICANT: Panichelli, Christophe
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B*8 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5756
; CURRENT APPLICATION NUMBER: US/10/164,078A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-078A-14

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x US-10-164-078A-14 (1-9)

QY 522 TCCTGTGTGATGATCAGCAGTGC 548
DB 1 SerleuMetPrlrThrGlnCys 9

RESULT 165
US-10-164-078A-23
; Sequence 23, Application US/10164078A
; Publication No. US20030228325A1
; GENERAL INFORMATION:
; APPLICANT: Bilsborough, Janine
; APPLICANT: Schultz, Erwin
; APPLICANT: Panichelli, Christophe
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B*8 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5756
; CURRENT APPLICATION NUMBER: US/10/164,078A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 23
; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-078A-23

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-164-078A-23 (1-9)

QY 327 CTCGGCATGCCCTTGGCAGACCCATG 353
|||||
DB 1 LeuAlaMetProPheAlaThrProMet 9

RESULT 166
US-10-164-078A-24
; Sequence 24, Application US/10164078A
; Publication No. US20030228325A1
; GENERAL INFORMATION:
; APPLICANT: Bilsborough, Janine
; APPLICANT: Schultz, Erwin
; APPLICANT: Panichelli, Christophe
; APPLICANT: Van der Bruggen, Pierre
; APPLICANT: Boon, Thierry
; TITLE OF INVENTION: Isolated Peptides Which Bind to HLA-B*8 Molecules And Uses Thereof
; FILE REFERENCE: LUD-5756
; CURRENT APPLICATION NUMBER: US/10/164, 078A
; CURRENT FILING DATE: 2002-06-05
; NUMBER OF SEQ ID NOS: 35
; SEQ ID NO 24
; LENGTH: 9
; TYPE: PRT
; ORGANISM: H. sapiens
; FEATURE:
US-10-164-078A-24

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-164-078A-24 (1-9)

QY 291 GCCAGGGGGCGGAGAGCCGCTGCTT 317
|||||
DB 1 AlaArgGlyProGluSerArgLeuLeu 9

RESULT 167
US-10-447-161-37
; Sequence 37, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 37
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-37

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0

DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-447-161-37 (1-9)

QY 522 TCCTGTGATGTGATCAGCAGTGC 548
|||||
DB 1 SerLeuMetIleThrGlnCys 9

RESULT 168
US-10-447-161-38
; Sequence 38, Application US/10447161
; Publication No. US20040023314A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Rong-fu
; TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
; FILE REFERENCE: HO-P02484US1
; CURRENT APPLICATION NUMBER: US/10/447,161
; CURRENT FILING DATE: 2003-05-28
; PRIOR APPLICATION NUMBER: 60/383,530
; PRIOR FILING DATE: 2002-05-28
; NUMBER OF SEQ ID NOS: 148
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 38
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-447-161-38

Alignment Scores:
Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-447-161-38 (1-9)

QY 516 CAGCTTCCCTGTGTGATGTGATCAG 542
|||||
DB 1 GlnLeuSerLeuMetIleThr 9

RESULT 169
US-10-706-475-2
; Sequence 2, Application US/10706475
; Publication No. US20040077548A1
; GENERAL INFORMATION:
; APPLICANT: Cerundolo, Vincenzo
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629.1
; CURRENT APPLICATION NUMBER: US/10/706,475
; CURRENT FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: US/09/514,036E
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 09/440,621
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 09/165,546
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: US 09/062,422
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 08/725,162
; PRIOR FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 2
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-475-2

Alignment Scores:
Pred. No.: 267 Length: 9

Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-706-475-2 (1-9)

Qy 522 TCCCTGTGATGTGATCAGCAGTGC 548
Db 1 SerLeuSeMetTrpIleThrGlnCys 9

RESULT 170

US-10-706-475-3
; Sequence 3, Application US/10706475
; Publication No. US2004007548A1
; GENERAL INFORMATION:
; APPLICANT: Cerundolo, Vincenzo
; TITLE OF INVENTION: Derivatives of NY-ESO-1 Peptides and Uses Thereof
; FILE REFERENCE: LUD 5629.1
; CURRENT APPLICATION NUMBER: US/10/706,475
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: US/09/514,036E
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: US 09/440,621
; PRIOR FILING DATE: 1999-11-15
; PRIOR APPLICATION NUMBER: US 09/165,546
; PRIOR FILING DATE: 1998-10-02
; PRIOR APPLICATION NUMBER: US 09/062,422
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: US 08/725,162
; PRIOR FILING DATE: 1996-10-03
; NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 3
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-706-475-3

Alignment Scores:

Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-706-475-3 (1-9)

Qy 516 CAGCTTCCCTGTGATGTGATCAGC 542
Db 1 GlnLeuSeMetTrpIleThr 9

RESULT 171

US-10-777-053-12
; Sequence 12, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: MANRK.022C1
; CURRENT APPLICATION NUMBER: US/10/777,053
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-777-053-12

Alignment Scores:

Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-777-053-12 (1-9)

Qy 522 TCCCTGTGATGTGATCAGCAGTGC 548
Db 1 SerLeuSeMetTrpIleThrGlnCys 9

RESULT 172

US-10-777-053-14
; Sequence 14, Application US/10777053
; Publication No. US20040132088A1
; GENERAL INFORMATION:
; APPLICANT: Simard, John J. L.
; APPLICANT: Diamond, David C.
; APPLICANT: Qiu, Zhiyong
; APPLICANT: Lei, Xiang-Dong
; TITLE OF INVENTION: EXPRESSION VECTORS ENCODING EPITOPES OF
; FILE REFERENCE: TARGET-ASSOCIATED ANTIGENS AND METHODS FOR THEIR DESIGN
; CURRENT APPLICATION NUMBER: US/10/777,053
; PRIOR FILING DATE: 2004-02-10
; PRIOR APPLICATION NUMBER: 10/292,413
; PRIOR FILING DATE: 2002-11-07
; PRIOR APPLICATION NUMBER: 60/336,968
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 979
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-777-053-14

Alignment Scores:

Pred. No.: 267 Length: 9
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 5.00% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-777-053-14 (1-9)

Qy 540 ACGCAGTGTTCGCGCCGCTTTTGG 566
Db 1 ThrGlnCysPheLeuProValPheLeu 9

RESULT 173

US-10-313-986-493
; Sequence 493, Application US/10313986
; Publication No. US20030236209A1
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tonglong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19

```
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 493
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-493

Alignment Scores:
Pred. No.:          92.6      Length:      20
Score:              9.00      Matches:      9
Percent Similarity: 50.00%    Conservative: 0
Best Local Similarity: 50.00% Mismatches:    9
Query Match:        5.06%     Indels:       0
DB:                 1         Gaps:         0

US-10-023-182-1 (1-752) x US-10-313-986-493 (1-20)

OY      157  CCGGCGCGCGCATGCGCCCGCGCATGCAGGATCCAGGGCCTCGTGGG 104
DB      1  ProglytleProabpGlyProglyGlyasnAlaglyGlyProglyGlyAlagly 18

RESULT 174
US-10-236-734-1402
; Sequence 1402, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1402
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLA segment 3
US-10-236-734-1402

Alignment Scores:
Pred. No.:          77.9      Length:      30
Score:              9.00      Matches:      9
Percent Similarity: 37.50%    Conservative: 0
Best Local Similarity: 37.50% Mismatches:    15
Query Match:        5.06%     Indels:       0
DB:                 1         Gaps:         0

US-10-023-182-1 (1-752) x US-10-296-734-1402 (1-30)

OY      220  GCGCCCGAGGCGCTTGCGCCCGCGCGGAGACTTGCGCCCGCGTGGACCCGCC 161
DB      5  GlyProglyGlyAlaGlyAlaThrGlyGlyArgGlyProArgGlyAlaGlyAlaAlaArg 24

OY      160  TCTCTGCGGCGG 149
DB      25  AlaserGlyPro 28

RESULT 175
US-10-236-734-1424
; Sequence 1424, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
```

```
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1424
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLB segment 2
US-10-236-734-1424

Alignment Scores:
Pred. No.:          77.9      Length:      30
Score:              9.00      Matches:      9
Percent Similarity: 42.86%    Conservative: 0
Best Local Similarity: 42.86% Mismatches:    12
Query Match:        5.06%     Indels:       0
DB:                 1         Gaps:         0

US-10-023-182-1 (1-752) x US-10-236-734-1424 (1-30)

OY      519  GCTGCTGAGACAGAGAGCTGAGAGAGCTGAGCGGTGCTGCAGACAGTCAGTC 460
DB      6  AlalalagIngluarGargValProArgAlaAlaGluValProglyAlaGInglyInglIn 25

OY      459  GGA 457
DB      26  Gly 26

RESULT 176
US-10-236-734-1426
; Sequence 1426, Application US/10296734
; Publication No. US20040054137A1
; GENERAL INFORMATION:
; APPLICANT: Thompson, Scott A
; APPLICANT: Ramshaw, Ian A
; TITLE OF INVENTION: Synthetic molecules and uses therefor
; FILE REFERENCE: Savine
; CURRENT APPLICATION NUMBER: US/10/296,734
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: AU PQ7761/00
; PRIOR FILING DATE: 2000-05-26
; NUMBER OF SEQ ID NOS: 1507
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1426
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: NYSOLB segment 3
US-10-236-734-1426

Alignment Scores:
Pred. No.:          77.9      Length:      30
Score:              9.00      Matches:      9
Percent Similarity: 33.33%    Conservative: 0
Best Local Similarity: 33.33% Mismatches:    18
Query Match:        5.06%     Indels:       0
DB:                 1         Gaps:         0

US-10-023-182-1 (1-752) x US-10-236-734-1426 (1-30)

OY      298  CCCCTGGCGCCGATGTCAGACATTCATGAGCCGCGCGCCATGCGGACCC 239
DB      4  ProglyAlaGInglyInglInglyProArgGlyArgGluGluAlaProArgGlyValArg 23

OY      238  GCGGCGCGCCTCTCCCGGC 218
DB      24  MetAlaAlaArgLeuGIngly 30
```

RESULT 177
US-10-117-937-180
; Sequence 180, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPTOPE SEQUENCES
; FILE REFERENCE: CTILIM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 180
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-180

Alignment Scores:
Pred. No.: 300 Length: 8
Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.44% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-180 (1-8)

QY 399 CTCCCGTCCAGGGGTCTCTG 422
Db 1 LeuProValProGlyValLeuLeu 8

RESULT 178
US-10-117-937-184
; Sequence 184, Application US/10117937
; Publication No. US20030220239A1
; GENERAL INFORMATION:
; APPLICANT: CTL IMMUNO THERAPIES CORP.
; APPLICANT: SIMARD, John, J.L.
; APPLICANT: DIAMOND, David, C.
; APPLICANT: LIU, Liping
; APPLICANT: XIE, Zhidong
; TITLE OF INVENTION: EPTOPE SEQUENCES
; FILE REFERENCE: CTILIM.027A
; CURRENT APPLICATION NUMBER: US/10/117,937
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,211
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/337,017
; PRIOR FILING DATE: 2001-11-07
; PRIOR APPLICATION NUMBER: US 60/363,210
; PRIOR FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 602
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 184
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-937-184

Alignment Scores:
Pred. No.: 300 Length: 8

Score: 8.00 Matches: 8
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.44% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x US-10-117-937-184 (1-8)

QY 399 CTCCCGTCCAGGGGTCTCTG 422
Db 1 LeuProValProGlyValLeuLeu 8

Search completed: July 21, 2004, 11:05:45
Job time : 3.5 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_blue_n2p model

Run on: July 21, 2004, 10:59:59 ; Search time 1.5 seconds
(without alignments)
4.086 Million cell updates/sec

Title: US-10-023-182-1
Perfect score: 180
Sequence: 1 ATGCAGCCGCAAGGCGCGG.....CTCCCTCAGGCGCAGAGGCGC 540

Scoring table: UNITARY_AA
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 490 seqs, 5675 residues
Total number of hits satisfying chosen parameters: 980

Minimum DB seq length: 5
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 499 summaries

Command line parameters:
-MODEL=frame+ n2p model -DEV=soft -O=pending Patente NA Main:US-10-023-182-1
-DB=rag1.pbp -SUFFIX=ptc -OUT=davis182-1.rag -MINMATCH=0.1 -LOOPECL=0
-LOOPEXT=0 -UNITS=bits -START=54 -END=593 -MATRIX=unitary_AA
-TRANS=Numen40.cdi -LIST=499 -DOCALIGN=200 -THR SCORE=Pct -THR MAX=100
-THR MIN=0 -ALIGN=499 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500
-MINLEN=5 -MAXLEN=50 -NCPU=6 -NO XLPXY -NEG SCORES=0 -LONGLOG -THREADS=1
-XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6
-DELEXT=7

Database : rag1.pbp:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	16.7	30	AAU85104	Human NYNSOLA segm
2	30	16.7	30	AAU85111	Human NYNSOLA segm
3	30	16.7	30	AAU85108	Human NYNSOLA segm
4	30	16.7	30	AAU85109	Human NYNSOLA segm
5	30	16.7	30	AAU85119	Human NYNSOLA segm
6	30	16.7	30	AAU85105	Human NYNSOLA segm
7	30	16.7	30	AAU85116	Human NYNSOLA segm
8	30	16.7	30	AAU85106	Human NYNSOLA segm
9	30	16.7	30	AAU85103	Human NYNSOLA segm
10	30	16.7	30	AAU85115	Human NYNSOLA segm
11	30	16.7	30	AAU85107	Human NYNSOLA segm
12	30	16.7	30	AAU85112	Human NYNSOLA segm
13	30	16.7	30	AAU85112	Human NYNSOLA segm
14	30	16.7	30	ABP74370	Human NY-ESO-1 pep
15	28	15.6	28	ABP74370	Human NY-ESO-1 pep
16	28	15.6	28	ABP74371	Human NY-ESO-1 pep
17	28	15.6	28	ADC09230	Human NY-ESO-1 pep
18	28	15.6	28	ADC09229	Human NY-ESO-1 pep
19	27	15.0	27	AAE07757	Human HLA-DP restr
20	27	15.0	27	AAE07717	Human NY-ESO-1 MHC

21	25	13.9	25	1	AAE07718	Human NY-ESO-1 MHC
22	25	13.9	25	1	ADD71521	HLA-DP4 binding pe
23	25	13.9	25	1	ADD71522	HLA-DP4 binding pe
24	25	13.9	25	1	ADD71532	HLA-DP4 binding pe
25	23	12.8	23	1	ADD71520	HLA-DP4 binding pe
26	21	11.7	21	1	ADD71449	Human cancer antiq
27	20	11.1	20	1	AAU05979	Human ESO p156-175
28	20	11.1	20	1	AAE07744	Human ESO p111-130
29	20	11.1	20	1	AAE07746	Human ESO p131-150
30	20	11.1	20	1	AAE07743	Human NY-ESO-1 MHC
31	20	11.1	20	1	AAE07731	Human NY-ESO-1 MHC
32	20	11.1	20	1	AAE07729	Human NY-ESO-1 MHC
33	20	11.1	20	1	AAE07742	Human ESO p126-145
34	20	11.1	20	1	AAE07747	Human ESO p91-101
35	20	11.1	20	1	AAE07741	Human ESO p82-101
36	20	11.1	20	1	AAE07732	Human NY-ESO-1 MHC
37	20	11.1	20	1	AAE07745	Human ESO p146-165
38	20	11.1	20	1	ADD71448	HLA-DP4 binding pe
39	18	10.0	18	1	AAU52435	Human tumour antiq
40	18	10.0	18	1	AAU52439	Human tumour antiq
41	18	10.0	18	1	AAU52438	Human tumour antiq
42	18	10.0	18	1	AAU52440	Human tumour antiq
43	18	10.0	18	1	AAU69941	Human NY-ESO-1 HLA
44	18	10.0	18	1	AAU69942	Human NY-ESO-1 HLA
45	18	10.0	18	1	AAU69940	Human NY-ESO-1 HLA
46	18	10.0	18	1	AAU69944	Human NY-ESO-1 HLA
47	18	10.0	18	1	AAU69943	Human NY-ESO-1 HLA
48	18	10.0	18	1	AAU69939	Human NY-ESO-1 HLA
49	18	10.0	18	1	AAU01539	HLA-DR53 recognist
50	18	10.0	18	1	AAU01543	HLA-DR53 recognist
51	18	10.0	18	1	AAU01544	HLA-DR53 recognist
52	18	10.0	18	1	AAU01542	HLA-DR53 recognist
53	18	10.0	18	1	AAU01540	HLA-DR53 recognist
54	18	10.0	18	1	AAU01541	HLA-DR53 recognist
55	18	10.0	18	1	AAU07769	Human NY-ESO-1 HLA
56	18	10.0	18	1	AAE07770	Human NY-ESO-1 HLA
57	18	10.0	18	1	ABG79132	Human NY-ESO-1 cla
58	18	10.0	18	1	ADD35557	Human NY-ESO-1 pep
59	18	10.0	18	1	ADD35555	Human NY-ESO-1 pep
60	18	10.0	18	1	ADD35556	Human NY-ESO-1 pep
61	17	9.4	17	1	AAE07719	Human NY-ESO-1 MHC
62	17	9.4	17	1	AAE07753	Human NY-ESO-1 MHC
63	17	9.4	17	1	AAE07735	Human NY-ESO-1 MHC
64	17	9.4	17	1	AAE07738	Human NY-ESO-1 MHC
65	16	8.9	16	1	AAE07779	Human NY-ESO-1 pep
66	16	8.9	16	1	AAE07720	Human NY-ESO-1 MHC
67	15	8.3	15	1	AAU05978	Human cancer antiq
68	15	8.3	15	1	AAU01550	Human NY-ESO-1 tum
69	15	8.3	15	1	AAE07721	Human NY-ESO-1 MHC
70	15	8.3	15	1	AAE07726	Human NY-ESO-1 MHC
71	15	8.3	15	1	AAE07780	Human NY-ESO-1 pep
72	15	8.3	15	1	AAE07727	Human NY-ESO-1 MHC
73	15	8.3	15	1	AAE07786	Human NY-ESO-1 pep
74	15	8.3	15	1	AAE07787	Human NY-ESO-1 pep
75	15	8.3	15	1	AAE07748	Human NY-ESO-1 pep
76	15	8.3	15	1	ADD71533	HLA-DP4 binding pe
77	14	7.8	14	1	AAU05986	Human cancer antiq
78	14	7.8	14	1	AAU01549	Human NY-ESO-1 tum
79	14	7.8	14	1	AAE07762	Human HLA-DP restr
80	14	7.8	14	1	AAE07740	Human NY-ESO-1 MHC
81	14	7.8	14	1	AAE07772	Human NY-ESO-1 pep
82	14	7.8	14	1	AAE07788	Human NY-ESO-1 pep
83	14	7.8	14	1	AAE07764	Human HLA-DP restr
84	14	7.8	14	1	AAE07722	Human NY-ESO-1 MHC
85	14	7.8	14	1	AAE07763	Human HLA-DP restr
86	14	7.8	14	1	AAE07766	Human HLA-DP restr
87	14	7.8	14	1	AAE07728	Human NY-ESO-1 MHC
88	14	7.8	14	1	AAE07758	Human NY-ESO-1 pro
89	14	7.8	14	1	AAE07771	Human NY-ESO-1 pep
90	14	7.8	14	1	AAE07736	Human NY-ESO-1 MHC
91	14	7.8	14	1	AAE07765	Human HLA-DP restr
92	14	7.8	14	1	AAE07775	Human NY-ESO-1 pep
93	14	7.8	14	1	AAE07749	Human NY-ESO-1 pep

94	14	7.8	14	1	AAE07759	Human HLA-DP restr	167	10	5.6	10	1	AAV06008	Human cancer anti
95	14	7.8	14	1	AAE07773	Human NY ESO-1 pep	168	10	5.6	10	1	AAV06055	AAV06055
96	14	7.8	14	1	AAE07774	Human NY ESO-1 pep	169	10	5.6	10	1	AAV06069	Human cancer anti
97	14	7.8	14	1	AAE07761	Human HLA-DP restr	170	10	5.6	10	1	AAV05992	Human cancer anti
98	14	7.8	14	1	AAE07781	Human NY ESO-1 pep	171	10	5.6	10	1	AAV05998	Human cancer anti
99	13	7.2	13	1	AAV05985	Human cancer anti	172	10	5.6	10	1	AAV06009	Human cancer anti
100	13	7.2	13	1	AAV06064	Human cancer anti	173	10	5.6	10	1	AAV05989	Human cancer anti
101	13	7.2	13	1	AAE07750	Human NY ESO-1 pep	174	10	5.6	10	1	AAV06004	Human cancer anti
102	13	7.2	13	1	AAE07776	Human NY ESO-1 pep	175	10	5.6	10	1	AAV06017	Human cancer anti
103	13	7.2	13	1	AAE07737	Human NY ESO-1 MHC	176	10	5.6	10	1	AAV05988	Human cancer anti
104	13	7.2	13	1	AAE07723	Human NY ESO-1 MHC	177	10	5.6	10	1	AAV06001	Human cancer anti
105	13	7.2	13	1	AAE07782	Human NY ESO-1 pep	178	10	5.6	10	1	AAV06007	Human cancer anti
106	12	6.7	12	1	AAV06065	Human cancer anti	179	10	5.6	10	1	AAV06057	Human cancer anti
107	12	6.7	12	1	AAV05984	Human cancer anti	180	10	5.6	10	1	AAV06060	Human cancer anti
108	12	6.7	12	1	AAE07724	Human NY ESO-1 MHC	181	10	5.6	10	1	AAV06002	Human cancer anti
109	12	6.7	12	1	AAE07783	Human NY ESO-1 pep	182	10	5.6	10	1	AAV06056	Human cancer anti
110	12	6.7	12	1	AAE07751	Human NY ESO-1 pep	183	10	5.6	10	1	AAV52434	Human cancer anti
111	11	6.1	11	1	AAW62585	Cancer associated	184	10	5.6	10	1	AAV70836	Human tumour anti
112	11	6.1	11	1	AAV05983	Human cancer anti	185	10	5.6	10	1	AAV70858	Human cancer anti
113	11	6.1	11	1	AAV06068	Human cancer anti	186	10	5.6	10	1	AAV70858	Human cancer anti
114	11	6.1	11	1	AAV06066	Human cancer anti	187	10	5.6	10	1	AAV79762	Human cancer anti
115	11	6.1	11	1	AAV01761	Exemplary antigen	188	10	5.6	10	1	AAV79759	Human cancer anti
116	11	6.1	11	1	AAV52431	Human tumour anti	189	10	5.6	10	1	AAV79760	Human cancer anti
117	11	6.1	11	1	AAE22730	NY-ESO-1 peptide e	190	10	5.6	10	1	AAE69927	Human NY-ESO-1 HLA
118	11	6.1	11	1	AAV70855	CTL epitope-1 of h	191	10	5.6	10	1	AAE69929	Human NY-ESO-1 HLA
119	11	6.1	11	1	AAV78469	NY-ESO-1 derived p	192	10	5.6	10	1	AAE69933	Human NY-ESO-1 HLA
120	11	6.1	11	1	AAE02630	Tumour associated	193	10	5.6	10	1	AAE69936	Human NY-ESO-1 HLA
121	11	6.1	11	1	AAE08702	Antigenic peptide	194	10	5.6	10	1	AAE69935	Human NY-ESO-1 HLA
122	11	6.1	11	1	AAE02119	NY-ESO-1 human leu	195	10	5.6	10	1	AAE69932	Human NY-ESO-1 HLA
123	11	6.1	11	1	AAE69947	Human NY-ESO-1 CTL	196	10	5.6	10	1	AAE69937	Human NY-ESO-1 HLA
124	11	6.1	11	1	AAE67165	Cancer testis tumo	197	10	5.6	10	1	AAE69925	Human NY-ESO-1 HLA
125	11	6.1	11	1	AAU01536	Cycolytic T cell 1	198	10	5.6	10	1	AAE69926	Human NY-ESO-1 HLA
126	11	6.1	11	1	AAE31327	Exemplary antigen	199	10	5.6	10	1	AAE69934	Human NY-ESO-1 HLA
127	11	6.1	11	1	AAE31328	Exemplary antigen	200	10	5.6	10	1	AAE69928	Human NY-ESO-1 HLA
128	11	6.1	11	1	AAE85298	HLA-A2 binding NY-	201	10	5.6	10	1	AAE69930	Human NY-ESO-1 HLA
129	11	6.1	11	1	AAE82016	HLA-A2 binding pep	202	10	5.6	10	1	AAE67195	Cancer testis tumo
130	11	6.1	11	1	AAE07752	Human NY ESO-1 pep	203	10	5.6	10	1	AAE67203	Cancer testis tumo
131	11	6.1	11	1	AAE07784	Human NY ESO-1 pep	204	10	5.6	10	1	AAE67204	Cancer testis tumo
132	11	6.1	11	1	AAE07725	Human NY ESO-1 MHC	205	10	5.6	10	1	AAE67196	Cancer testis tumo
133	11	6.1	11	1	AAE07777	Human wildtype NY	206	10	5.6	10	1	AAE67205	Cancer testis tumo
134	11	6.1	11	1	AAE06849	Human NY-ESO-1 ant	207	10	5.6	10	1	AAE67201	Cancer testis tumo
135	11	6.1	11	1	ABG66804	Tumour antigen LAG	208	10	5.6	10	1	AAE67197	Cancer testis tumo
136	11	6.1	11	1	ABU64812	Human NY-ESO-1 CTL	209	10	5.6	10	1	AAE67200	Cancer testis tumo
137	11	6.1	11	1	ADA19552	Human cancer anti	210	10	5.6	10	1	AAE67194	Cancer testis tumo
138	11	6.1	11	1	ADD35559	Human NY-ESO-1 pep	211	10	5.6	10	1	AAE67202	Cancer testis tumo
139	11	6.2	30	1	AAU85119	Human LAGE1 segmen	212	10	5.6	10	1	AAE67193	Cancer testis tumo
C 140	11	6.2	30	1	AAU85105	Human NYNSOla segm	213	10	5.6	10	1	AAE67198	Cancer testis tumo
C 141	11	6.2	30	1	AAU85103	Human NYNSOla segm	214	10	5.6	10	1	AAE67545	Human complementar
142	10	5.6	10	1	AAV06059	Human cancer anti	215	10	5.6	10	1	AAE693818	Human complementar
143	10	5.6	10	1	AAV06062	Human cancer anti	216	10	5.6	10	1	AAE697546	Human complementar
144	10	5.6	10	1	AAV05982	Human cancer anti	217	10	5.6	10	1	AAE31331	Exemplary antigen
145	10	5.6	10	1	AAV05996	Human cancer anti	218	10	5.6	10	1	AAE31332	Exemplary antigen
146	10	5.6	10	1	AAV06014	Human cancer anti	219	10	5.6	10	1	AAE85307	HLA-A2 binding NY-
147	10	5.6	10	1	AAV06011	Human cancer anti	220	10	5.6	10	1	AAE07734	Human MHC class I
148	10	5.6	10	1	AAV06058	Human cancer anti	221	10	5.6	10	1	AAE07785	Human NY ESO-1 pep
149	10	5.6	10	1	AAV05999	Human cancer anti	222	10	5.6	10	1	AAE07778	Human NY ESO-1 pep
150	10	5.6	10	1	AAV06010	Human cancer anti	223	10	5.6	10	1	AAE07730	Human NY ESO-1 MHC
151	10	5.6	10	1	AAV06012	Human cancer anti	224	10	5.6	10	1	ABE79072	Human CAMEL class
152	10	5.6	10	1	AAV05991	Human cancer anti	225	10	5.6	10	1	ABG79130	Human NY-ESO-1 cla
153	10	5.6	10	1	AAV06006	Human cancer anti	226	10	5.6	10	1	ABG66803	Tumour antigen NY-
154	10	5.6	10	1	AAV06013	Human cancer anti	227	10	5.6	10	1	ABG66802	Tumour antigen NY-
155	10	5.6	10	1	AAV05990	Human cancer anti	228	10	5.6	10	1	ABP74299	Human NY-ESO-1 pep
156	10	5.6	10	1	AAV06016	Human cancer anti	229	10	5.6	10	1	ABP74302	Human NY-ESO-1 pep
157	10	5.6	10	1	AAV05994	Human cancer anti	230	10	5.6	10	1	ABP74317	Human NY-ESO-1 pep
158	10	5.6	10	1	AAV05997	Human cancer anti	231	10	5.6	10	1	ABP74295	Human NY-ESO-1 pep
159	10	5.6	10	1	AAV06003	Human cancer anti	232	10	5.6	10	1	ABP74292	Human NY-ESO-1 pep
160	10	5.6	10	1	AAV06015	Human cancer anti	233	10	5.6	10	1	ABP74287	Human NY-ESO-1 pep
161	10	5.6	10	1	AAV06063	Human cancer anti	234	10	5.6	10	1	ABP74474	Human NY-ESO-1 pep
162	10	5.6	10	1	AAV05980	Human cancer anti	235	10	5.6	10	1	ABP74297	Human NY-ESO-1 pep
163	10	5.6	10	1	AAV05969	Human cancer anti	236	10	5.6	10	1	ABP74473	Human NY-ESO-1 pep
164	10	5.6	10	1	AAV05993	Human cancer anti	237	10	5.6	10	1	ABP74291	Human NY-ESO-1 pep
165	10	5.6	10	1	AAV06000	Human cancer anti	238	10	5.6	10	1	ABP74304	Human NY-ESO-1 pep
166	10	5.6	10	1	AAV06005	Human cancer anti	239	10	5.6	10	1	ABP74307	Human NY-ESO-1 pep

240	10	5.6	10	1	ABP74310	Human NY-ESO-1 epi	313	9	5.0	9	1	AAV06033	Human cancer antiig
241	10	5.6	10	1	ABP74311	Human NY-ESO-1 epi	314	9	5.0	9	1	AAV06047	Human cancer antiig
242	10	5.6	10	1	ABP74319	Human NY-ESO-1 epi	315	9	5.0	9	1	AAV01763	Exemplary antigeni
243	10	5.6	10	1	ABU64848	Human NY-ESO-1 HLA	316	9	5.0	9	1	AAV01762	Exemplary antigeni
244	10	5.6	10	1	ABU64843	Human NY-ESO-1 HLA	317	9	5.0	9	1	AAV52433	Human tumour antiig
245	10	5.6	10	1	ABU64853	Human NY-ESO-1 HLA	318	9	5.0	9	1	AAV52432	Human tumour antiig
246	10	5.6	10	1	ABU64852	Human NY-ESO-1 HLA	319	9	5.0	9	1	AAV52432	Human tumour antiig
247	10	5.6	10	1	ABU64851	Human NY-ESO-1 HLA	320	9	5.0	9	1	AAV70857	CAMEL10 immunogeni
248	10	5.6	10	1	ABU64842	Human NY-ESO-1 HLA	321	9	5.0	9	1	AAV70859	CAMEL17 immunogeni
249	10	5.6	10	1	ABU64841	Human NY-ESO-1 HLA	322	9	5.0	9	1	AAV79749	NY-ESO-1 derived p
250	10	5.6	10	1	ABU64845	Human NY-ESO-1 HLA	323	9	5.0	9	1	AAV79748	NY-ESO-1 derived p
251	10	5.6	10	1	ABU64846	Human NY-ESO-1 HLA	324	9	5.0	9	1	AAV79750	NY-ESO-1 derived p
252	10	5.6	10	1	ABU64844	Human NY-ESO-1 HLA	325	9	5.0	9	1	AAV79755	NY-ESO-1 derived p
253	10	5.6	10	1	ABU64850	Human NY-ESO-1 HLA	326	9	5.0	9	1	AAV79757	NY-ESO-1 derived p
254	10	5.6	10	1	ADC09161	Epitope with high	327	9	5.0	9	1	AAV79753	NY-ESO-1 derived p
255	10	5.6	10	1	ADC09150	Epitope with high	328	9	5.0	9	1	AAV79756	NY-ESO-1 derived p
256	10	5.6	10	1	ADC09176	Epitope with high	329	9	5.0	9	1	AAV78466	NY-ESO-1 derived p
257	10	5.6	10	1	ADC09151	Epitope with high	330	9	5.0	9	1	AAV79751	NY-ESO-1 derived p
258	10	5.6	10	1	ADC09163	Epitope with high	331	9	5.0	9	1	AAV79754	NY-ESO-1 derived p
259	10	5.6	10	1	ADC09170	Epitope with high	332	9	5.0	9	1	AAV78471	NY-ESO-1 derived p
260	10	5.6	10	1	ADC09346	Epitope with high	333	9	5.0	9	1	AAV79758	NY-ESO-1 derived p
261	10	5.6	10	1	ADC09142	Epitope with high	334	9	5.0	9	1	AAV78465	NY-ESO-1 derived p
262	10	5.6	10	1	ADC09154	Epitope with high	335	9	5.0	9	1	AAV78470	NY-ESO-1 derived p
263	10	5.6	10	1	ADC09156	Epitope with high	336	9	5.0	9	1	AAV79752	NY-ESO-1 derived p
264	10	5.6	10	1	ADC09178	Epitope with high	337	9	5.0	9	1	ABW02832	Tumour associated
265	10	5.6	10	1	ADC09169	Epitope with high	338	9	5.0	9	1	ABW02631	Tumour associated
266	10	5.6	10	1	ADC09166	Epitope with high	339	9	5.0	9	1	ABW08703	Antigenic peptide
267	10	5.6	10	1	ADC09333	Epitope with high	340	9	5.0	9	1	ABW08704	Antigenic peptide
268	10	5.6	10	1	ADC09158	Epitope with high	341	9	5.0	9	1	AAW99363	Vaccine related MH
269	10	5.6	10	1	ADD35567	Human NY-ESO-1 pep	342	9	5.0	9	1	AAE02120	NY-ESO-1 human leu
270	10	5.6	10	1	ADD35562	Human NY-ESO-1 pep	343	9	5.0	9	1	AAE02121	NY-ESO-1 human leu
271	10	5.6	30	1	AAU85106	Human NYNSO1a segm	344	9	5.0	9	1	AAW69910	Human NY-ESO-1 HLA
C 272	10	5.6	30	1	AAU85107	Human NYNSO1a segm	345	9	5.0	9	1	AAW69911	Human NY-ESO-1 HLA
C 273	10	5.6	30	1	ADD35566	Human NY-ESO-1 pep	346	9	5.0	9	1	AAW69914	Human NY-ESO-1 HLA
2													

386	9	5.0	9	1	AA667170	Cancer testis tumo
387	9	5.0	9	1	AA667174	Cancer testis tumo
388	9	5.0	9	1	AA667184	Cancer testis tumo
389	9	5.0	9	1	AA667187	Cancer testis tumo
390	9	5.0	9	1	AA667182	Cancer testis tumo
391	9	5.0	9	1	AA667192	Cancer testis tumo
392	9	5.0	9	1	AAU01546	Human NY-ESO-1 tum
393	9	5.0	9	1	AAU01545	Human NY-ESO-1 tum
394	9	5.0	9	1	AAU01537	Cytolytic T cell 1
395	9	5.0	9	1	AA631330	Exemplary antigen
396	9	5.0	9	1	AA631329	Exemplary antigen
397	9	5.0	9	1	AA685299	HLA-A2 binding NY-
398	9	5.0	9	1	AA685300	HLA-A2 binding NY-
399	9	5.0	9	1	AA682017	HLA- binding pepci
400	9	5.0	9	1	AA682018	HLA- binding pepci
401	9	5.0	9	1	AA606850	Human NY-ESO-1 ant
402	9	5.0	9	1	AA606851	Human NY-ESO-1 ant
403	9	5.0	9	1	AA626810	Human HLA-A2.1 res
404	9	5.0	9	1	AA626808	Human HLA-A2.1 res
405	9	5.0	9	1	AAO21432	Isolated peptide f
406	9	5.0	9	1	AAO21431	Isolated peptide f
407	9	5.0	9	1	AAO21430	HLA-A2 restricted
408	9	5.0	9	1	AAE31113	Human ctag peptide
409	9	5.0	9	1	AAE31112	Human ctag peptide
410	9	5.0	9	1	AAE31114	Human ctag peptide
411	9	5.0	9	1	AAE31115	Human ctag peptide
412	9	5.0	9	1	AAE31110	Human ctag peptide
413	9	5.0	9	1	AAE31171	Human ctag peptide
414	9	5.0	9	1	AAE31371	Human CTAG peptide
415	9	5.0	9	1	ABP74293	Human NY-ESO-1 epi
416	9	5.0	9	1	ABP74313	Human NY-ESO-1 epi
417	9	5.0	9	1	ABP74309	Human NY-ESO-1 epi
418	9	5.0	9	1	ABP74318	Human NY-ESO-1 epi
419	9	5.0	9	1	ABP74298	Human NY-ESO-1 epi
420	9	5.0	9	1	ABP74306	Human NY-ESO-1 epi
421	9	5.0	9	1	ABP74286	Human NY-ESO-1 epi
422	9	5.0	9	1	ABP74294	Human NY-ESO-1 epi
423	9	5.0	9	1	ABP74308	Human NY-ESO-1 epi
424	9	5.0	9	1	ABP74315	Human NY-ESO-1 epi
425	9	5.0	9	1	ABP74290	Human NY-ESO-1 epi
426	9	5.0	9	1	ABP74301	Human NY-ESO-1 epi
427	9	5.0	9	1	ABP74303	Human NY-ESO-1 epi
428	9	5.0	9	1	ABP74288	Human NY-ESO-1 epi
429	9	5.0	9	1	ABP74285	Human NY-ESO-1 epi
430	9	5.0	9	1	ABP74314	Human NY-ESO-1 epi
431	9	5.0	9	1	ABP74289	Human NY-ESO-1 epi
432	9	5.0	9	1	ABP74472	Human NY-ESO-1 epi
433	9	5.0	9	1	ABP74316	Human NY-ESO-1 epi
434	9	5.0	9	1	ABP74312	Human NY-ESO-1 epi
435	9	5.0	9	1	ABP74471	Human NY-ESO-1 epi
436	9	5.0	9	1	ABP74305	Human NY-ESO-1 epi
437	9	5.0	9	1	ABP74470	Human NY-ESO-1 epi
438	9	5.0	9	1	ABU64827	Human NY-ESO-1 HLA
439	9	5.0	9	1	ABU64824	Human NY-ESO-1 HLA
440	9	5.0	9	1	ABU64831	Human NY-ESO-1 HLA
441	9	5.0	9	1	ABU64832	Human NY-ESO-1 HLA
442	9	5.0	9	1	ABU64838	Human NY-ESO-1 HLA
443	9	5.0	9	1	ABU64817	Human NY-ESO-1 HLA
444	9	5.0	9	1	ABU64834	Human NY-ESO-1 HLA
445	9	5.0	9	1	ABU64630	Human NY-ESO-1 HLA
446	9	5.0	9	1	ABU64630	Human NY-ESO-1 HLA
447	9	5.0	9	1	ABU64840	Human NY-ESO-1 HLA
448	9	5.0	9	1	ABU64835	Human NY-ESO-1 HLA
449	9	5.0	9	1	ABU64813	Human NY-ESO-1 CTL
450	9	5.0	9	1	ABU64818	Human NY-ESO-1 HLA
451	9	5.0	9	1	ABU64828	Human NY-ESO-1 HLA
452	9	5.0	9	1	ABU64822	Human NY-ESO-1 HLA
453	9	5.0	9	1	ABU64825	Human NY-ESO-1 HLA
454	9	5.0	9	1	ABU64836	Human NY-ESO-1 HLA
455	9	5.0	9	1	ABU64839	Human NY-ESO-1 HLA
456	9	5.0	9	1	ABU64814	Human NY-ESO-1 CTL
457	9	5.0	9	1	ABU64823	Human NY-ESO-1 HLA
458	9	5.0	9	1	ABU64819	Human NY-ESO-1 HLA

459	9	5.0	9	1	ABU64826	Human NY-ESO-1 HLA
460	9	5.0	9	1	ADA19553	Human cancer antig
461	9	5.0	9	1	ADA19554	Human cancer antig
462	9	5.0	9	1	ADC08165	Epitope with high
463	9	5.0	9	1	ADC08147	Epitope with high
464	9	5.0	9	1	ADC08160	Epitope with high
465	9	5.0	9	1	ADC08157	Epitope with high
466	9	5.0	9	1	ADC08162	Epitope with high
467	9	5.0	9	1	ADC08148	Epitope with high
468	9	5.0	9	1	ADC08149	Epitope with high
469	9	5.0	9	1	ADC08172	Epitope with high
470	9	5.0	9	1	ADC08329	Epitope with high
471	9	5.0	9	1	ADC08167	Epitope with high
472	9	5.0	9	1	ADC08145	Epitope with high
473	9	5.0	9	1	ADC08152	Epitope with high
474	9	5.0	9	1	ADC08171	Epitope with high
475	9	5.0	9	1	ADC08175	Epitope with high
476	9	5.0	9	1	ADC08330	Epitope with high
477	9	5.0	9	1	ADC08173	Epitope with high
478	9	5.0	9	1	ADC08174	Epitope with high
479	9	5.0	9	1	ADC08153	Epitope with high
480	9	5.0	9	1	ADC08164	Epitope with high
481	9	5.0	9	1	ADC08168	Epitope with high
482	9	5.0	9	1	ADC08144	Epitope with high
483	9	5.0	9	1	ADC08177	Epitope with high
484	9	5.0	9	1	ADC08331	Epitope with high
485	9	5.0	9	1	ADD35553	Human NY-ESO-1 pep
486	9	5.0	9	1	ADD35554	Human NY-ESO-1 pep
487	9	5.0	9	1	ADD35554	Human NY-ESO-1 pep
488	9	5.0	9	1	ADD35552	Human NY-ESO-1 pep
489	9	5.0	9	1	ADD35558	Human NY-ESO-1 pep
490	9	5.0	9	1	ADD35560	Human NY-ESO-1 pep
491	9	5.0	9	1	AAU85104	Human NYNSO1a segm
492	9	5.1	30	1	AAU85116	Human NYNSO1b segm
493	9	5.1	30	1	AAU85115	Human NYNSO1b segm
494	9	5.1	30	1	AAU85115	Human NYNSO1b segm
495	8	4.4	8	1	AAU85115	Human NYNSO1b segm
496	8	4.4	8	1	ABP74296	Human cancer antig
497	8	4.4	8	1	ABP74300	Human NY-ESO-1 epi
498	8	4.4	8	1	ADC08155	Human NY-ESO-1 epi
499	8	4.4	8	1	ADC08159	Epitope with high

ALIGNMENTS

RESULT 1	
ID	AAU85104 standard; peptide; 30 AA.
XX	AAU85104;
AC	
XX	
DT	08-MAY-2002 (first entry)
XX	
DE	Human NYNSO1a segment 3.
XX	
KW	Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW	viral infection; human immunodeficiency virus; melanoma;
KW	bacterial infection; Salmonella; Legionella; parasitic infection;
KW	Trypanosoma; Toxoplasma; Giardia.
XX	
OS	Homo sapiens.
XX	
PN	WC000190197-A1.
XX	
PD	29-NOV-2001.
XX	
PF	25-MAY-2001; 2001WC-AU000622.
XX	
PR	26-MAY-2000; 2000AU-00007761.
XX	
PA	(AUSU) UNIV AUSTRALIAN NAT.
XX	
PI	Thomson SA, Ramshaw IA;

```
XX WPI: 2002-147575/19.
DR N-PSDB; ABK36924.
XX
PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
PS Example 3; Fig 27; 364pp; English.
XX
CC The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium) or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
SQ Sequence 30 AA;
XX
Alignment Scores:
Pred. No.: 4.25 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x AAU85104 (1-30)
QY 138 GGCATGCTGGCGGCCGAGAGCGGGTGCACAGGCGGCGAGAGTCCCGGGGCGCA 197
Db 1 Glyenmlaaglygylproglgylualaglylathrglygylalrglproalrglyala 20
QY 198 GGGGACAGAGGGCGCTCGGGGCGGAGGA 227
Db 21 Glyalalalargalaserglyproglygly 30
RESULT 2
AAU85111
XX AAU85111 standard; peptide; 30 AA.
XX
AC AAU85111;
XX
DT 08-MAY-2002 (first entry)
XX
DE Human NTRNSOLA segment 10.
XX
XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
XX viral infection; human immunodeficiency virus; melanoma;
XX bacterial infection; Salmonella; Legionella; parasitic infection;
XX Trypanosoma; Toxoplasma; Giardia.
XX
OS Homo sapiens.
XX
PN WO200190197-A1.
```

```
XX
PD 29-NOV-2001.
XX
XX 25-MAY-2001; 2001WO-AUD000622.
XX
XX 26-MAY-2000; 2000AU-00007761.
XX
XX (AUSU ) UNIV AUSTRALIAN NAT.
XX
XX Thomson SA, Ramshaw IA;
XX
DR WPI: 2002-147575/19.
DR N-PSDB; ABK36931.
XX
PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
PS Example 3; Fig 27; 364pp; English.
XX
CC The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium) or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
SQ Sequence 30 AA;
XX
Alignment Scores:
Pred. No.: 4.25 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x AAU85111 (1-30)
QY 453 ACTATCCGACTGACTGTGTCAGACACCGGCAACTGACGCTTTCATCAGCTCTGTCTC 512
Db 1 ThrileargleuthralaalaasphlaasrglneuglneuserlieserCysleu 20
QY 513 CAGCAGCTTCCTCGTGGATGATCAGC 542
Db 21 Glndlnleuserleuuewetrpillethr 30
RESULT 3
AAU85108
XX AAU85108 standard; peptide; 30 AA.
XX
AC AAU85108;
XX
DT 08-MAY-2002 (first entry)
XX
```

DE Human NYNSOLA segment 7.
XX
KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficiency virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
OS Homo sapiens.
XX
PN WO200190197-A1.
XX
PD 29-NOV-2001.
XX
PF 25-MAY-2001; 2001WO-AU000622.
XX
PR 26-MAY-2000; 2000AU-00007761.
XX
PA (AUSU) UNIV AUSTRALIAN NAT.
XX
PI Thomson SA, Ramshaw IA;
XX
DR WPI; 2002-147575/19.
XX
DR N-PSDB; ABK36928.
XX
PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
PS Example 3; Fig 27; 364pp; English.
XX
XX The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptide. The synthetic polypeptide is useful for
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
SQ Sequence 30 AA;
XX
Alignment Scores:
Pred. No.: 4.25 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x AAU85108 (1-30)
QY 318 GAATTCTACCTGCGCATGECCTTTGCGCAACCCATGAGAGAGAGCTGCCCGAGAGAGC 377
Db 1 GIupherytyleuAlamecProphenalathrPrometGuaIaGluAlaAArgser 20
QY 378 CTGGCCGAGATGCCCGACCGCTTCCGCTG 407
|||||

Db 21 LeuAlaGlnsPaIaProPoleuProVal 30
RESULT 4
AAU85109
ID AAU85109 standard; peptide; 30 AA.
XX
XX AAU85109;
AC
XX
DT 08-MAY-2002 (first entry)
XX
DE Human NYNSOLA segment 8.
XX
KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficiency virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
XX
OS Homo sapiens.
XX
PN WO200190197-A1.
XX
PD 29-NOV-2001.
XX
PF 25-MAY-2001; 2001WO-AU000622.
XX
PR 26-MAY-2000; 2000AU-00007761.
XX
PA (AUSU) UNIV AUSTRALIAN NAT.
XX
PI Thomson SA, Ramshaw IA;
XX
DR WPI; 2002-147575/19.
XX
DR N-PSDB; ABK36928.
XX
PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
PS Example 3; Fig 27; 364pp; English.
XX
XX The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
SQ Sequence 30 AA;
XX
Alignment Scores:
Pred. No.: 4.25 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0

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DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x AAU85109 (1-30)
QY 363 CTGCCCCGAGAGACCTGGCCAGAGATGCCCGCTTCCCGCCAGGGGAGTCTTCTG 422
    |||
Db 1 LeuAlaArgArgSerLeuAlaGlnAspAlaProProLeuProValProGlyValLeuLeu 20
    |||
QY 423 AAGGATTCACGTGTGTCGGCAGCATACTG 452
    |||
Db 21 LysGluPheThrValSerGlyAsnIleLeu 30
    |||

RESULT 5
AAU85119
ID AAU85119 standard; peptide; 30 AA.
XX
AC AAU85119;
XX
DT 08-MAY-2002 (first entry)
DE Human LAGE1 segment 2.
XX
KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficiency virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
XX
OS Homo sapiens.
XX
PN WO200190197-A1.
XX
PD 29-NOV-2001.
XX
PF 25-MAY-2001; 2001WO-AU000622.
XX
PR 26-MAY-2000; 2000AU-00007761.
XX
PA (AUSU ) UNIV AUSTRALIAN NAT.
XX
PI Thomson SA, Ramshaw IA;
XX
DR WPI; 2002-147575/19.
XX
DR N-PSDB; ABK36939.
XX
PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
PS Example 3; Fig 27; 364pp; English.
XX
CC The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium) or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
```

```
CC invention
XX
SQ Sequence 30 AA;
XX
Alignment Scores:
Pred. No.: 4.25 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0

US-10-023-182-1 (1-752) x AAU85119 (1-30)
QY 93 GATGCTGATGCGCCAGAGGCGCTGGCATCTCGATGAGCCAGGAGGAGCATGCGCGC 152
    |||
Db 1 AspAlaAspGlyProGlyGlyProGlyIleProAspGlyProGlyGlyAsnAlaGlyGly 20
    |||
QY 153 CCAGAGAGGCGGATGCGCCAGCGGCGCAGA 182
    |||
Db 21 ProGlyGluAlaGlyAlaThrGlyGlyArg 30
    |||

RESULT 6
AAU85105
ID AAU85105 standard; peptide; 30 AA.
XX
AC AAU85105;
XX
DT 08-MAY-2002 (first entry)
DE Human NYNSOIA segment 4.
XX
KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficiency virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
XX
OS Homo sapiens.
XX
PN WO200190197-A1.
XX
PD 29-NOV-2001.
XX
PF 25-MAY-2001; 2001WO-AU000622.
XX
PR 26-MAY-2000; 2000AU-00007761.
XX
PA (AUSU ) UNIV AUSTRALIAN NAT.
XX
PI Thomson SA, Ramshaw IA;
XX
DR WPI; 2002-147575/19.
XX
DR N-PSDB; ABK36925.
XX
PT New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
PS Example 3; Fig 27; 364pp; English.
XX
CC The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
```



```
XX New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
XX Example 3; Fig 27; 364pp; English.
XX
CC The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium) or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
SQ Sequence 30 AA;
XX
Alignment Scores:
Pred. No.: 4.25 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0
XX
US-10-023-182-1 (1-752) x AAU85110 (1-30)
XX
QY 408 CCAGGGGCTTTCGAGGAGTTCATCGTGTCCGCAACATATGACTATCGACT 467
DB 1 ProGlyValLeuLeuLysGluPheThrValSerGlySerGlnLeuThrIleArgLeuThr 20
XX
QY 468 GCTGCAGACCAACCGCAACTGCAGCTCTCC 497
DB 21 AlaIleAlaPheIleArgGlnLeuGlnLeuSer 30
XX
RESULT 9
AAU85106
ID AAU85106 standard; peptide; 30 AA.
XX
AC AAU85106;
XX
DT 08-MAY-2002 (first entry)
DE Human NYNSOLA segment 5.
XX
KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KM viral infection; human immunodeficiency virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
XX
OS Homo sapiens.
XX
XX WO200190197-A1.
XX
XX 29-NOV-2001.
XX
```

```
PF 25-MAY-2001; 2001WO-AU000622.
XX
XX 26-MAY-2000; 2000AU-00007761.
PR
XX (AUSU ) UNIV AUSTRALIAN NAT.
XX
XX Thomson SA, Ramshaw IA;
XX
XX WPI: 2002-147575/19.
DR N-PSDB: ABK3692C.
XX
XX New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
XX Example 3; Fig 27; 364pp; English.
XX
XX The invention relates to a new synthetic polypeptide (I) comprising
XX several different segments of at least one parent polypeptide linked
XX together in a different relationship relative to their linkage in the
XX parent polypeptide to impede, abrogate or otherwise alter at least one
XX function associated with the parent polypeptide and for inducing an
XX immune response against a pathogen or cancer. Also included are a
XX synthetic polynucleotide encoding and a computer system for designing the
XX synthetic polypeptides. The synthetic polypeptides and polynucleotides
XX are referred to as a Savine. The synthetic polypeptide is useful for
XX modulating immune responses preferably directed against a pathogen or a
XX cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
XX and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
XX oesophagus, brain, testicle, uterus), as potentiating agents.
XX Compositions comprising the polypeptide may be used in the treatment or
XX prophylaxis against viral (such as infections caused by HIV (human
XX immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
XX virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
XX (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
XX Salmonella, Streptococcal, Legionella and Mycobacterium) or parasitic
XX (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
XX Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
XX a peptide derived from a parent protein used to construct a savine of the
XX invention
XX
SQ Sequence 30 AA;
XX
Alignment Scores:
Pred. No.: 4.25 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0
XX
US-10-023-182-1 (1-752) x AAU85106 (1-30)
XX
QY 228 GGCGCCCCGGGGGCTTCGATGCGGGCGGGCTTCGATGATGATGCTGCAGATGC 287
DB 1 GlyAlaProArgGlyProHisGlyGlyAlaIleSerGlyLeuSerGlySerGlyArgCys 20
XX
QY 288 GGAGCCAGGGGGCCGAGAGCCGCTGCTT 317
DB 21 GlyAlaArgGlyProGlnSerArgLeuLeu 30
XX
RESULT 10
AAU85103
ID AAU85103 standard; peptide; 30 AA.
XX
AC AAU85103;
XX
DT 08-MAY-2002 (first entry)
DE Human NYNSOLA segment 2.
XX
KW Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
```

KW viral infection; human immunodeficiency virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
OS Homo sapiens.
XX WO200190197-A1.
XX
XX
XX 29-NOV-2001.
XX
XX 25-MAY-2001; 2001WO-AU000622.
XX
XX 26-MAY-2000; 2000AU-00007761.
PR
XX (AUSU) UNIV AUSTRALIAN NAT.
XX
XX Thomson SA, Ramshaw IA;
PI
XX
XX MPI. 2002-147575/19.
DR N-PSDB; ABRK36923.
XX
XX
XX New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
XX
XX Example 3; Fig 27; 364pp; English.
XX
XX
XX The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
XX
SQ Sequence 30 AA;
Alignment Scores:
Pred. No.: 4.25 Length: 30
Score: 100.00% Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
Gaps: 0
DB: 1
US-10-023-182-1 (1-752) x AAU85103 (1-30)

QY 93 GATGCTGATGGCCCAAGAGCCCTGATTCCTGATGGCCAGGGAGCATCTGGCGC 152
DB 1 AepalaaepgilyProglyllepToaaepgilyProglylGlyAaahlaaely 20
QY 153 CCAAGAGAGCGCGGTGCCACGGCGCGCAGA 182
DB 21 ProglylGluAaGlyAlaThrGlyGlyArg 30

RESULT 11

AAU85115
ID AAU85115 standard; peptide; 30 AA.
AC
XX AAU85115;
XX
XX 08-MAY-2002 (first entry)
XX
XX Human NYNSOLB segment 2.
DE
XX
XX Savine; vaccine; cancer; viral infection; HIV; hepatitis C virus;
KW viral infection; human immunodeficiency virus; melanoma;
KW bacterial infection; Salmonella; Legionella; parasitic infection;
KW Trypanosoma; Toxoplasma; Giardia.
XX
XX Homo sapiens.
XX
XX WO200190197-A1.
XX
XX
XX 29-NOV-2001.
XX
XX 25-MAY-2001; 2001WO-AU000622.
XX
XX 26-MAY-2000; 2000AU-00007761.
PR
XX (AUSU) UNIV AUSTRALIAN NAT.
XX
XX Thomson SA, Ramshaw IA;
PI
XX
XX MPI. 2002-147575/19.
DR N-PSDB; ABRK36935.
XX
XX
XX New synthetic polypeptides having several different segments of at least
PT one parent polypeptide linked together differently compared to the
PT linkage in the parent polypeptide, for inducing immune response against a
PT pathogen or cancer.
XX
XX
XX Example 3; Fig 27; 364pp; English.
XX
XX
XX The invention relates to a new synthetic polypeptide (I) comprising
CC several different segments of at least one parent polypeptide linked
CC together in a different relationship relative to their linkage in the
CC parent polypeptide to impede, abrogate or otherwise alter at least one
CC function associated with the parent polypeptide and for inducing an
CC immune response against a pathogen or cancer. Also included are a
CC synthetic polynucleotide encoding and a computer system for designing the
CC synthetic polypeptides. The synthetic polypeptides and polynucleotides
CC are referred to as a Savine. The synthetic polypeptide is useful for
CC modulating immune responses preferably directed against a pathogen or a
CC cancer, (e.g., cancers of the lung, breast, ovary, cervix, colon, head
CC and neck, pancreas, prostate, stomach, bladder, kidney, bone liver,
CC oesophagus, brain, testicle, uterus), as potentiating agents.
CC Compositions comprising the polypeptide may be used in the treatment or
CC prophylaxis against viral (such as infections caused by HIV (human
CC immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a savine of the
CC invention
XX
XX
SQ Sequence 30 AA;
Alignment Scores:
Pred. No.: 4.25 Length: 30
Score: 100.00% Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
Gaps: 0
DB: 1
US-10-023-182-1 (1-752) x AAU85115 (1-30)

immunodeficiency virus), hepatitis, influenza, Japanese encephalitis
CC virus, Epstein-Barr virus and respiratory syncytial virus), bacterial
CC (e.g., infections caused by Neisseria, Meningococcal, Haemophilus,
CC Salmonella, Streptococcal, Legionella and Mycobacterium or parasitic
CC (e.g., infections caused by Plasmodium, Schistosoma, Leishmania,
CC Trypanosoma, Toxoplasma and Giardia) infections. The present sequence is
CC a peptide derived from a parent protein used to construct a vaccine of the
CC invention
SQ Sequence 30 AA;
Alignment Scores:
Pred. No.: 4.25 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x AAU85112 (1-30)
QY 498 ATCAGCTCCTGTCCTCAGAGCTTCCCTGTTGATGGATCAGCAGTCTTCTGACC 557
DB 1 11eSerSerCysLeuGlnGlnLeuSerLeuMetTrpIleThrGlnCysPheLeuPro 20
QY 558 GTGTTTGGCTCAGCCTCCCTCAGGAG 587
DB 21 ValPheLeuAlaGlnProProSerGlyGln 30
RESULT 14
ADD35566
ID ADD35566 standard; peptide; 30 AA.
XX
AC ADD35566;
XX
DT 15-JAN-2004 (first entry)
XX
DE Human NY-ESO-1 peptide SEQ ID NO:16.
XX
KW human leukocyte antigen; HLA; cytolytic T cell stimulator;
KW immune response; cytostatic; gene therapy; human; NY-ESO-1;
KW immunogenic tumour antigen.
XX
OS Homo sapiens.
XX
PN WO2003068600-A2.
XX
PD 21-AUG-2003.
XX
PF 12-FEB-2003; 2003WO-US004182.
XX
PR 13-FEB-2002; 2002US-0355828P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Jager E, Knuth A, Old L, Gnjatic S;
XX
DR WPI; 2003-902684/82.
XX
PT New isolated peptide that binds to an HLA molecule, useful for treating a
PT subject with a disorder characterized by the presence of complexes of an
PT HLA molecule and the peptide, e.g. cancer, and for inducing immune
PT response.
XX
PS Example 9; SEQ ID NO 16; 73pp; English.
XX
CC The present invention describes an isolated peptide (1) consisting of 8-
CC 11, which binds to a human leukocyte (HLA) molecule, e.g. an HLA-A3, HLA-
CC B35 or an HLA-B51 molecule, and stimulates cytolytic T cells specific for
CC complexes of the peptide and the HLA molecule, where at least 8
CC contiguous amino acids of the peptide consist of at least 8 contiguous
CC amino acid sequence of p94-102, p93-101, p108-116 or p91-99. Also
CC described: (1) a composition comprising (1) and a carrier; (2) an

isolated nucleic acid molecule encoding (1) or the polypeptide; (3) an
CC expression vector comprising the nucleic acid of (2) in operable linkage
CC with a promoter; (4) a host cell transformed with the nucleic acid of (2)
CC or the expression vector of (3); (5) an isolated cytolytic T-cell (CTL)
CC specific for a complex of the HLA molecule and (1); (6) detecting the CTL
CC of (5); (7) a polypeptide comprising at least two of (1) that are linked
CC together; (8) an isolated nucleic acid that encodes the polypeptide; (9) an
CC isolated tetramer comprising the HLA molecule, biotin and a binding
CC partner; (10) a composition comprising the tetramer and a carrier; (11)
CC inducing an immune response in a subject; (12) treating a subject with a
CC disorder characterised by the presence of complexes of an HLA molecule
CC and the peptide; (13) a combinatorial library of derivatives of (1),
CC where the derivatives consist of 8-11 amino acids; (14) a screening assay
CC for an analogue of (1); (15) an isolated antibody or its fragment that
CC specifically binds a HLA/peptide complex, or (1); (16) an isolated
CC soluble T cell receptor that specifically binds to a HLA/peptide complex;
CC and (17) inducing an immune response on a subject having a disorder
CC characterised by the presence of the HLA molecule and the peptide. (1)
CC has cytostatic activity, and can be used in gene therapy. The peptides,
CC nucleic acid molecules, vectors, compositions, antibodies and methods are
CC useful for treating a subject with a disorder characterised by the
CC presence of complexes of an HLA molecule and the peptide, and for
CC inducing an immune response. The present sequence represents a human NY-
CC ESO-1 peptide, which is used in the exemplification of the present
CC invention. NY-ESO-1 is an immunogenic tumour antigen.
SQ Sequence 30 AA;
Alignment Scores:
Pred. No.: 4.25 Length: 30
Score: 30.00 Matches: 30
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 16.67% Indels: 0
DB: 1 Gaps: 0
US-10-023-182-1 (1-752) x ADD35566 (1-30)
QY 291 GCCAGGGGCGCGAGAGCCGCTGCTGAGTCTACCTCGCCATGCTTCGACGACACC 350
DB 1 AlaArgGlyProGlnSerArgLeuGlnPheThrLeuAlaMetProPheAlaThrPro 20
QY 351 ATGGAAGCAGAGCTGCGCCCGCAGGAGCGCTG 380
DB 21 MetGlnAlaGlnLeuAlaArgArgSerLeu 30
RESULT 15
ABP74370
ID ABP74370 standard; peptide; 28 AA.
XX
AC ABP74370;
XX
DT 03-FEB-2003 (first entry)
XX
DE Human NY-ESO-1 epitope SEQ ID NO:254.
XX
KW Human; epitope; vaccine; immunotherapeutic; cytostatic; immunogenicity;
KW T cell.
XX
OS Homo sapiens.
XX
PN WO200281646-A2.
XX
PD 17-OCT-2002.
XX
PF 04-APR-2002; 2002WO-US011101.
XX
PR 06-APR-2001; 2001US-0282211P.
XX
PR 07-NOV-2001; 2001US-0337017P.
XX
PR 07-MAR-2002; 2002US-0363210P.
XX
PA (CTL1-) CTL IMMUNOTHERAPIES CORP.
XX